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Search completed: September 22, 2004, 07:02:53 Job time : 34 secs
                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                            LENGTH: 6 amino acids
                                                                                                                                                                                                                                                                                                              amino acid
GY: both
                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                           US-08-924-002-1
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APPLICANT: Ruoglahti, Erkki
APPLICANT: Koivunen, Erkki
TITLE OF INVENTION: No. 5981478el Integrin-Binding Peptides
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 35; DB 2; Length 6; 100.0%; Pred. No. 3e+05; Ative 0; Mismatches 0; Indels
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; Sequence 1, Application US/08924002
; Patent No. 6177542
; GENERAL INFORMATION:
    APPLICANT: Revolute, Erkki I.
    APPLICANT: Rolvunen, Erkki
; TITLE OF INVENTION: NOVEL INTEGRIN-BINDING PEPTIDES;
    NUMBER OF SEQUENCES: 26
    CORRESPONDENES 26
; ADDRESSEE: Campbell & Flores LLP
    STREET: 4370 La Jolla Village Drive, Suite 700
    CITYE: San Diego
    STATE: California
; COUNTRY: USA
                                                                                                                                                                                                                            ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PARENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/286,861
FILING DATE: 04-AUG-1994
CLASSIFICATION NUMBER: US 08/158,001
FILING DATE: 4-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAMME: Campbell, Cathryn
REGISTRATION NUMBER: P-LA 9992
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-9001
TELEFROMATION FOR SEQ ID NO: 7:
CROMPATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/924,002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/625,695
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Best Local Similarity 100...
5; Conservative
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US-08-924-002-1
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Gaps
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                                                                                                                    NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LA 2748
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-9001
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
FILING DATE: 03-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/212,186
FILING DATE: 11-WAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
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Query Match 100.0%; Score 35; DB 2; Length 6; Best Local Similarity 100.0%; Pred. No. 3e+05; Matches 5; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 25, Application US/08625695A
Fatent No. 591234
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
MUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
MUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
STREET: 4770 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             UPERMILIUS SYSTEM: EV-LUDS/MS-LUDS
SOFFWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/625,695A
FILING DATE: 03-APR-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/212,186
FILING DATE: 11-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,915
REFERENCE/DOCKET NUMBER: P-LA 2041
TELEPHONE: (619) 535-8949
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
TEMBERS (619) 535-8949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 35; DB 2;
100.0%; Pred. No. 3e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                          SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
    INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                           amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                     US-08-625-695A-26
                                                                                               ; TOPOLOGY:
US-08-625-695A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-625-695A-26
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US-08-286-861-7
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COMPUTER: FLORM:
MEDIUM TYPE: FLORM disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/625,695A
FILING DATE: 03-APR-1996
CLASSIFICATION 1530
PRIOR APPLICATION 1530
PRIOR APPLICATION THORER: US 08/212,186
FILING DATE: 11-MAR-1994
ATTONNEY/AGENT INPORMATION:
NAME: Campbell, Cathyn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: 9-LA 2041
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAME: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Ruoslahti, Erkki I.
APPLICANT: Roivunen, Erkki
TITLE OF INVENTION: NOVEL INTEGRIN-BINDING PEPTIDES
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSE: CAMPBELL & FLORES, LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/425,238
FILING DATE:
                                                                                                                                                                                                                            CLASSIFICATION: 514
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/158,001
FILLING DATE: 24-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: 9-LA 9775
TELEPONNUNICATION INFORMATION:
TELEPONE: (619) 535-9001
TELEPAX: (619) 535-901
TELEPAX: (619) 535-901
TELEPAX: (619) 535-901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/08625695A Patent No. 5912234 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
                   ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TOPOLOGY: linear
US-08-425-238-4
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US-08-625-695A-1
COUNTRY:
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B: Campbell and Flores
4370 La Jolla Village Drive, Suite 700
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                          Score 35; DB 1;
Pred. No. 3e+05;
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Pred. No. 3e+05;
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                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: "CONTREMENT APPLICATION NUMBER: US/08/212,186A
FILING DATE: 11-MAR.1994
CLASSIFICATION NUMBER: US/08/212,186A
ATTORNEY/AGENT INFORMATION:
NAME: CAMDDEIL, CARINTYN A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LA 9861
TELECHONE: (619) 535-9001
TELECHONE: (619) 535-9001
TELERAX: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                         Sequence 26, Application US/08212186A Patent No. 5536814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/08425238 Patent No. 5627263
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100.0%;
                             100.0%;
                          Query Match
Best Local Similarity 100.
Matches 5; Conservative
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Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: San Diego
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
                                                                                                                               1 CRGDC 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT PAPLICATION DATA:

APPLICATION NUMBER: US/08/212,186A

FILING DATE: 11-MAR-1994

CLASSIPICATION: 514

ATTORNEY AGENT INFORMATION:

NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 315

REGISTRATION NUMBER: 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Rucelahti, Brkki I.
APPLICANT: Kojvunen, Brkki
TITLE OF INVENTION: NOVEL INTEGRIN-BINDING PEPTIDES
NUMBER OF SEQUENCES: 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                         NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/POCKET NUMBER: P-LA 2748
TELECOMUNICATION INFORMATION:
TELEPHONE: (619) 535-9091
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
                                                                                                  FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/625,695
FILING DATE: 03-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/212,186
FILING DATE: 11-MAR-1994
ATTORNEY/AGENT INFORMATION:
                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/924,002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 1, Application US/08212186A; Patent No. 5536814
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-8949
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
TOPOLOGY: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
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Best Local Similarity
Matches 5; Conserv
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Gaps
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APPLICANT: Rucelahti, Erkki
APPLICANT: Kolvinen, Erkki
TITLE OF INVENTION: No. 5627263el Integrin-Binding Peptides
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
0; Indels
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                                                                                                                                                                                                        Patent No. 5536814
GENERAL INFORMATION:
APPLICANT: Ruoslahti, Erkki I.
APPLICANT: Roolvunen, Erkki I.
APPLICANT: Kolvunen, Brkki
TITLE OF INVENTION: NOVEL INTEGRIN-BINDING PEPTIDES
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEE: Campbell and Flores: A370 La Jolla Village Drive, Suite 700 San Diego California
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TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
                                                                                                                circular
                                                                                   TYPE: amino acid
TOPOLOGY: circula
US-08-286-861-37
                                                                                                                                                                                                                                                        1 CRGDC 5
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                                                                                                                                   Sequence 35, Application US/08753781C
Sequence 35, Application US/08753781C
Sequence 35, Application US/08753781C
Sequence 35, Application US/08753781C
GENERAL INFORMATION:
APPLICANT: Markland Jr., Francis S.
APPLICANT: Bush, Larry R.
APPLICANT: Swenson, Stephen
APPLICANT: Plores Sanchez, Eladio
TITLE OF INVENTION: THROMBOLYTIC AGENTS WITH ANTITHROMBOTIC ACTIVITY
CURRENT APPLICATION NUMBER: US/08/753, 781C
NUMBER OF SEQ ID NOS: 40
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 35
LENGTH: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:synthetic
OTHER INFORMATION: peptide
US-08-753-781-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Ruoslahti, Erkki
APPLICANT: Koivunen, Erkki
TITLE OF INVENTION: No. 5981478el Integrin-Binding Peptides
CORRESPONDENCE ADDRESS:
ADDRESSEE: Gampbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.0%; Score 35; DB 2; Length 5; Best Local Similarity 100.0%; Pred. No. 3e+05; Matches 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/286,861
CLING DATE: 04-AUG-1994
CLIASSIFICATION: DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/158,001
FILING DATE: 24-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Campbell and Flores
4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RAISONING CATHYN
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LA 9992
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 37, Application US/08286861
Patent No. 5981478
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: San Diego
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CRGDC 5
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                                                                                                RESULT 5
US-08-753-781-35
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) FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:synthetic

US-09-141-127-15
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Query Match
100.0%; Score 35; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels
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i Sequence 10, Application US/08924002

i Sequence 10, Application US/08924002

i Sequence 10, Application US/08924002

i GENERAL INFORMATION:

APPLICANT: Ruoslahti, Erkki

APPLICANT: Koivunen, Erkki

ITITLE OF INVENTION: NOVEL INTEGRIN-BINDING PEPTIDES

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESSEE: Campbells Flores Lip

STREET: 4370 La Jolla Village Drive, Suite 700

STREET: California

COUNTRY: USA

ILIPITATE: CALIFORNIA

STREET: CALIFORNIA

COMPUTER READRALE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 15, Application US/09141127A
Fatent No. 6093481
GENERAL INFORMATION:
APPLICANT: Dean, Richard T.
APPLICANT: Lister-James, John
TITLE OF INVENTION: THROMBUS INAGING AGENTS
FILE REFERENCE: DIT 113.1USC:
CURRENT FPLING DATE: 1998-08-27
EARLIER APPLICATION NUMBER: 08/33,832
EARLIER APPLICATION NUMBER: 08/33,832
EARLIER APPLICATION NUMBER: 08/35,832
EARLIER FILING DATE: 1995-01-05
EARLIER FILING DATE: 1995-05-21
EARLIER FILING DATE: 1992-05-21
MUMBER OF SEQ ID NOS: 40
SOFTWARE: PATENT ON NUMBER: 07/886,752
NUMBER: OF SEQ ID NOS: 40
SOFTWARE: PATENT ON NUMBER: 07/886,752
MUMBER: DEBRIER FILING DATE: 1992-05-21
EARLIER FILING DATE: 1993-05-21
EARLIER FILING DATE: 1993-05-21
EARLIER FILING DATE: 1993-05-21
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03-APR-1996

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0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 35; DB 2; Length 5; 100.0%; Pred. No. 3e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Dean, Richard T
APPLICANT: Lister-James, John
TITLE OF INVENTION: Technetium-99m Labeled Peptides for
TITLE OF INVENTION: Thrombus Imaging
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMFUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

SOFTWARE: PATENT NAMBER: US/08/335,832

FILING DATE: 05-JAN-1995

CLASSIFICATION: 424

ATTORNEY/AGBNT INFORMATION:

NAME: No. 5925331nan, Kevin E

REFRENCE/DOCKET NUMBER: 35,303

REFRENCE/DOCKET NUMBER: 92,216-I

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Banner & Allegretti, Ltd.
STREET: 10 South Wacker Drive Suite 3000
STATE: Chicago
STATE: 111inois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                  US 08/212,186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 42, Application US/08335832
Patent No. 5925331
                                                                                                                              NAME: Campbell, Cathryn A.
REGISTRATION WUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LA.
TELECOMMUNICATION INFORMATION:
TELEFAX: (619) 535-9001
TELEFAX: (619) 535-9949
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                      FILING DATE: 11-MAR-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 312-715-1000
TELEFAX: 312-715-1234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 100.
Matches 5; Conservative
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                    5 amino acida
                     CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
                                                                                                                                                                                                                                                                                                                                            amino acid
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Best Local Similarity
Matches 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
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                     Patent No. 5627263
GENERAL INFORMATION:
APPLICANT: RUGISLALI, Erkki
APPLICANT: KOIVAIGH, Erkki
APPLICANT: KOIVAIGH, Erkki
TITLE OF INVENTION: No. 5627263e1 Integrin-Binding Peptides
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 35; DB 1; Length 5; 100.0%; Pred. No. 3e+05;
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Patent No. 5912234

GENERAL INFORMATION:

APPLICANT: Knoalahti, Erki I.

APPLICANT: Koivunen, Erki I.

APPLICANT: Koivunen, Erki

TITLE OF INVENTION: NOVEL INTEGRIN-BINDING PEPTIDES

NUMBER OF SOURCES: 27

CORRESPONDENCE ADDRESS:

ADDRESSER: CAMPBELL & FLORES, LLP

STREET: 4370 La Jolla Village Drive, Suite 700

CITY: San Diego

STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/425,238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READBABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/625,695A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/158,001
FILING DATE: 24-NOV-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                               COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LA
TELECOMMUNICATION INPORMATION:
TELEPANE: (619) 535-9001
TELEPAX: (619) 535-9001
INPORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
Sequence 8, Application US/08425238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    United States
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ss: single
linear
                                                                                                                                                                                                                            CITY: San Diego
STATE: California
COUNTRY: USA
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US-08-625-695A-10
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Best Loca Matches

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Sequence 10, Appli
Sequence 12, Appli
Sequence 21, Appli
Sequence 35, Appli
Sequence 37, Appli
Sequence 11, Appli
Sequence 10, Appli
Sequence 26, Appli
Sequence 26, Appli
Sequence 26, Appli
Sequence 27, Appli
Sequence 11, Appli
Sequence 26, Appli
Sequence 26, Appli
Sequence 11, Appli
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                                                                                         September 22, 2004, 06:51:52; Search time 32 Seconds (without alignments) 8.067 Million cell updates/sec
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Sequence
Sequence
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5: /cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
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US-08-425-238-8
US-08-425-695A-10
US-08-335-832-42
US-08-733-781-35
US-08-73-781-35
US-08-78-11-15
US-08-141-17-15
US-08-121-186A-10
US-08-212-186A-10
US-08-224-002-10
US-08-225-695A-1
US-08-225-695A-1
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US-08-286-861-15
US-08-286-861-15
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                                                             OM protein - protein search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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35
1 CRGDC 5
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Match Length
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Database :
                                                                                                                                                                                              Sequence:
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                                                                                              Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Result
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4, Appli 33, Appli 211, App 11, Appl 20, Appli 20, Appli 12, Appli 4, Appli 8, Appli 18, Appli 18, Appli 11, Appli 20, Appli 11, Appli 211, Appli 3, Appli 4, Appli 6, Appli 7, Appli 7, Appli 7, Appli 7, Appli 7, Appli 7, Appli 7, Appli 7, Appli 8, Appli 8, Appli 8, Appli 11, Appli 12, Appli 13, Appli 14, Appli 14, Appli 16, Appli 17, Appli 17, Appli 17, Appli 17, Appli 17, Appli 17, Appli 17, Appli 18, Appli 19, Appli 19, Appli 10, Appli 10, Appli 11, Appli 11		0 ;
2 2 3 3 4 4 4 9 4 9 9 9 9 9 9 9 9 9 9 9 9 9		Gaps
Sequence Seq		:0
28 35 100.0 9 3 US-09-130-225-4 See 35 100.0 9 3 US-09-134-671-33 See 31 35 100.0 9 3 US-09-134-671-33 See 31 35 100.0 9 3 US-09-139-602-1 See 32 100.0 9 3 US-09-130-0202-1 See 32 100.0 9 3 US-09-0426-680-12 See 32 100.0 9 4 US-09-455-681-3 See 32 100.0 9 4 US-09-455-681-3 See 32 100.0 9 4 US-09-455-681-3 See 32 100.0 9 4 US-09-174-943-8 See 32 100.0 9 4 US-09-174-943-8 See 32 100.0 9 4 US-09-15-127-18 See 41 35 100.0 9 4 US-09-15-127-18 See 41 35 100.0 9 4 US-09-15-127-18 See 41 35 100.0 9 4 US-09-12-250D-211 See 44 35 100.0 9 4 US-09-969-192-3 See 44 35 100.0 9 4 US-09-969-192-3 See 35 100.0 9 4 US-09-969-192-4 See 35 100.0 9 4 US-09-969-192-4	RESULT 1  US-08-212-186A-10  1 US-08-212-186A-10  1 Sequence 10, Application US/08212186A  2 Patent No. 5536814  APPLICANT: ROJANDEN, Erkki  1 TILE OF INVENTION: NOVEL INTEGRIN-BINDING PEPTIDES  CORRESSES CARDENS: 26  CORRESSES CARDENS: 26  CORRESSES CARDENS: 26  CORRESSES CARDENS: 36  CORRESSES CARDENS: 36  CITY: San Diego  STATE: 4370 La Jolla Village Drive, Suite 700  CITY: San Diego  CITY: San Diego  STATE: Callifornia  COMPUTR: IBM PC Compatible  COMPUTR: 1 DAR PC COMPATIBLE  COMPUTR: 1	Query Match 100.0%; Score 35; DB 1; Length 5; Best Local Similarity 100.0%; Pred. No. 3e+05; Matches 5; Conservative 0; Mismatches 0; Indels Qy 1 CRGDC 5

RESULT 2 US-08-425-238-8 THIS PAGE BLANK (USPTO)

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; SEQ ID NO 10
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FRATURE:
; OTHER INFORMATION: Synthetic Construct
; FRATURE:
; NAME/KEY: VARIANT
; OTHER INFORMATION: Alanine is attached to DSPE-PEGSK-succinyl
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Search completed: September 22, 2004, 07:04:03 Job time : 66 secs

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Genuence 14, Application US/09791524A

GENERAL INFORMATION:
APPLICANT: Aventis Pharmaceuticals Products Inc.
APPLICANT: Aventis Pharmaceuticals Products Inc.
TITLE OF INVENTION: Targeted Adenovirus Vectors For Delivery Of Heterologous Genes
TITLE OF INVENTION: Targeted Adenovirus Vectors For Delivery Of Heterologous Genes
TURE REFERENCE: P26,992-B USA
CURRENT APPLICATION NUMBER: US/09/791,524A
CURRENT APPLICATION NUMBER: PCT/1899/01524
PRIOR FILING DATE: 1999-08-27
PRIOR PLING DATE: 1999-08-27
PRIOR PLING DATE: 1998-08-27
NUMBER OF SEQ ID NOS: 165
SOFTWARE: Patentin version 3.2
SEQ ID NO 14
LENGTH: 11
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// Sequence 10, Application US/10850873

// APPLICANT: Paul, Ralph

// APPLICANT: Commore, Sally

// APPLICANT: Commore, Sally

// APPLICANT: Commore, Sally

// APPLICANT: Commore, Sally

// APPLICANT: O'Mahory, Daniel J.

// TITLE OF INVENTION: LIPID-COMPRISING DRUG DELIVERY COMPLEXES

// TITLE OF INVENTION: LIPID-COMPRISING DRUG DELIVERY COMPLEXES

// TITLE OF INVENTION: LIPID-COMPRISING DRUG DELIVERY COMPLEXES

// TITLE OF INVENTION: AND METHODS FOR THEIR PRODUCTION

// CURRENT APPLICATION NUMBER: US/10/136,187

// PRIOR APPLICATION NUMBER: US 60/287,786

// PRIOR PLING DATE: 2001-04-30

// WMBER OF SEQ ID NOS: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.0%; Score 35; DB 6; Length 10; Best Local Similarity 100.0%; Pred. No. 1.8; Matches 5; Conservative 0; Mismatches 0; Indels
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0; Mismatches
CURRENT APPLICATION NUMBER: US/10/808,758
CURRENT FILING DATE: 2004-03-24
PRIOR APPLICATION NUMBER: US 60/459,000
PRIOR PILING DATE: 2003-03-28
PRIOR PILING DATE: 2003-03-28
PRIOR PILING DATE: 2003-05-01
NUMBER OF SEQ ID NOS: 118
SOFTWARE: FRRESEQ for Windows Version 4.0
SEQ ID NO 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 35;
Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: cRGD peptide US-10-808-758-78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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; ORGANISM: Adenovirus
US-09-791-524A-14
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Best Local Similarity
Matches 5; Conserv
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US-09-791-524A-14
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GENERAL INFORMATION:
APPLICANT: Von Seggern, Daniel J.
TITLE OF INVENTION: ADENOVIRUS PARTICLES WITH ENHANCED INFECTIVITY OF DENDRITIC CELLS
TITLE OF INVENTION: PARTICLES WITH DECREASED INFECTIVITY OF HEPATOCYTES
FILE REFERENCE: 22908-1239
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US-10-712-298-20
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APPLICANT: Goodwin, Raymond G.
TITLE OF INVENTION: CYtokine that Induces Apoptosis
FILE REFERENCE: 2835-E
CURRENT APPLICATION NUMBER: US/10/712,298
CURRENT FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: US/09/796,581
PRIOR FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: 09/320,424
PRIOR APPLICATION NUMBER: 09/320,424
PRIOR APPLICATION NUMBER: 09/320,46
PRIOR APPLICATION NUMBER: 09/190,046
PRIOR APPLICATION NUMBER: 09/048,641
PRIOR APPLICATION NUMBER: 08/548,368
   PRIOR APPLICATION NUMBER: US 09/801,485
PRIOR FILING DATE: 2001-03-08
NUMBER OF SEQ ID NOS: 18
SCFTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 20, Application US/10712298 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                        OTHER INFORMATION: RGD Peptide US-10-917-709-2
                                                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 20
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Best Local Similarity
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0; Mismatches
PRIOR APPLICATION NUMBER: 09/190, 046
PRIOR FILING DATE: 1998-11-10
PRIOR PLING DATE: 1998-10-10
PRIOR PILING DATE: 1998-03-26
PRIOR PILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 08/670,354
PRIOR APPLICATION NUMBER: 08/548,368
PRIOR PILING DATE: 1995-11-01
PRIOR PILING DATE: 1995-11-01
PRIOR PILING DATE: 1995-16-29
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 2, Application US/10917709; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 5; Conservative
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Best Local Similarity 100.
Matches 5; Conservative
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US-10-917-709-2
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                                 GENERAL INFORMATION:
APPLICANT: Weng, Shaomeng
APPLICANT: Weng, Shaomeng
APPLICANT: Weng, Dajun
TITLE OF INVENTION: Small Molecule Antagonists of BCL-2 Family Proteins
FILE REFERENCE: UM-08477
CURRENT APPLICATION NUMBER: US/10/729,156
CURRENT FILING DATE: 2003-12-05
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
SEQ ID NO 4
LENGTH: 9
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                              Length 9;
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APPLICANT: Wiley, Seven R.
APPLICANT: Wiley, Seven R.
TITLE OF INVENTION: Cytokine that Induces Apoptosis; TITLE OF INVENTION: Cytokine that Induces Apoptosis; TITLE OF INVENTION: Cytokine that Induces Apoptosis; CURRENT FILING DATE: 2004-07-28; CURRENT FILING DATE: 2004-07-28; PRIOR APPLICATION NUMBER: US/09/796,581; PRIOR FILING DATE: 2001-02-27; PRIOR APPLICATION NUMBER: 09/320,424; PRIOR FILING DATE: 1999-05-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , OTHER INFORMATION: alpha-five integrin binding motif US-10-877-930-33
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APPLICANT: Hoe, Mee
TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
FILE REPRENCE: 31488
CURRENT APPLICATION NUMBER: US/10/877,930
CURRENT APPLICATION NUMBER: US/09/696,070
PRIOR APPLICATION NUMBER: US/09/696,070
PRIOR APPLICATION NUMBER: US/09/696,070
PRIOR APPLICATION NUMBER: US/09/696,070
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 33
LENGTH: 9
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                Sequence 4, Application US/10729156
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                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Synthetic
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Matches 5; Conservative
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Best Local Similarity
Matches 5; Conserv
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US-10-900-399-20
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APPLICANT: Dickerson, Erin B.
APPLICANT: Dickerson, Erin B.
APPLICANT: Helfand, Stuart C.
APPLICANT: Helfand, Stuart C.
APPLICANT: Akhtar, Nasim
TITLE OF INVENTION METHODS FOR TARGETING INTERLEUKIN-12 TO MALIGNANT ENDOTHELIUM
FILLE REFERENCE WARF-0025
CURRENT APPLICATION NUMBER: US/10/917,709
CURRENT FILING DATE: 2004-08-13
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US-10-912-764-34
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: artificial
FORTH OTHER INFORMATION: Peptide
08-10-900-399-20
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Sequence 34, Application US/10912764

GENERAL INFORMATION:
TITLE OF INVENTION: TARGETED CARRIER FUSIONS FOR DELIVERY OF TITLE OF INVENTION: CHEMOTHERAPEUTIC AGENTS
FILE REFERENCE: WARF:011US
CURRENT FILING DATE: 2004-08-05
PRIOR APPLICATION NUMBER: 60/492,508
PRIOR PILING DATE: 2003-08-05
PRIOR FILING DATE: 2003-08-05
NUMBER OF SEQ ID NOS: 63
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 34
LENGTH: 9
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                                                                                                                            100.0%; Score 35; DB 6; Length 9; 100.0%; Pred. No. 6.5e+05; Live 0; Mismatches 0; Indels
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APPLICANT: Heminway, Stuart J.
APPLICANT: Heminway, Stuart J.
APPLICANT: Liu, Shuang
APPLICANT: Liu, Shuang
APPLICANT: Singh, Patallad R.
TITLE OF INVENTION: PHARMACEUTICALS FOR THE IMAGING OF ANGIOGENIC DISORDERS
FILE REFERENCE: BMS-2024
CURRENT APPLICATION NUMBER: US/10/342,081
CURRENT FILING DATE: 2003-01-14
PRIOR FILING DATE: 2000-06-21
NUMBER: OF SEQ ID NOS: 169
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
SEQ ID NO 76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 35; DB 6; Le Similarity 100.0%; Pred. No. 6.5e+05; 5; Conservative 0; Mismatches 0;
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Rothman, James
APPLICANT: Rothman, James
APPLICANT: Maybew, Mark
APPLICANT: Hoe, Mee
TITUE OF INVENTION: FORE RECEPTOR INHIBITORS
FILE REFERENCE: 3148
CURRENT APPLICATION NUMBER: US/10/815,514
CURRENT APPLICATION NUMBER: US/09/696,872
FRIOR FILING DATE: 2004-03-31
PRIOR FILING DATE: 2000-10-26
NUMBER OF SEQ ID NOS: 42
SOFTWARE: FastSEQ for Windows Version 3.0
IENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     j OTHER INFORMATION: Synthetic Construct
US-10-342-081-76
                                                               US-10-342-081-76; Sequence 76, Application US/10342081; GENERAL INFORMATION:
                                                                                                                                                 APPLICANT: Edwards, D. Scott
APPLICANT: Barrett, John A.
APPLICANT: Carpenter, Jr., Alan P.
APPLICANT: Harris, Thomas D.
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
                                                                                                                                 APPLICANT: Rajopadhye, Milind
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Best Local Similarity
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US-10-815-514-33
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US-10-729-156-4
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APPLICANT: Aventis Pharmaceuticals Products Inc.
TITLE OF INVENTION: Targeted Adenovirus Vectors For Delivery Of Heterologous Genes FILE REFERENCE: P26,992-B USA
CURRENT APPLICATION NUMBER: US/09/791,524A
CURRENT FILING DATE: 2001-02-22
PRIOR APPLICATION NUMBER: US 60/098,028
PRIOR FILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: US 60/098,028
PRIOR FILING DATE: 1998-08-27
NUMBER OF SEQ ID NOS: 165
SOFTWARE: Patentin version 3.2
SEQ ID NO 124
                                                                                                                                                                                                                                                                                   Sequence 14, Application US/09612852A
GENERAL INFORMATION:
APPLICANT: CURIEL, DAVID T.
APPLICANT: KRASNYCH, VICTOR N.
TITLE OF INVENTION: MODIFIED ADENOVIRUS CONTAINING A FIBER REPLACEMENT PROTEIN
FILE REFERENCE: 678503-2006.2
CURRENT FILING DATE: 2000-07-10
PRIOR PLILOR DATE: 1999-02-16
PRIOR FILING DATE: 1999-02-16
PRIOR FILING DATE: 1999-02-17
NUMBER OF SEQ ID NOS: 20
SEQ ID NO 14
LENGTH: 9
LENGTH: 9
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                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Description of Unknown Organism: Peptide ligand OTHER INFORMATION: containing the RGD motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.0%; Score 35; DB 5; Length 9; Best Local Similarity 100.0%; Pred. No. 6.5e+05; Matches 5; Conservative 0; Mismatches 0; Indels
                                            DB 1; Length 9;
                                                                                       0; Indels
                                          100.0%; Score 35; DB 1; L
100.0%; Pred. No. 6.5e+05;
iive 0; Mismatches 0;
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8-09-791-524A-124
Sequence 124, Application US/09791524A
GENERAL INFORMATION:
                     Query Match
Best Local Similarity 100.
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US-09-791-524A-124
                                                                                                                                                             CRGDC 7
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US-09-612-852A-14
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PCT-US04-16382-7
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TYPE: PRT
CORGANISM: Adenovirus
US-09-791-524A-148
cképé 6
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PCT-US04-16382-7
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Sequence 7, Appli
Sequence 124, Appl
Sequence 35, Appl
Sequence 37, Appl
Sequence 37, Appl
Sequence 37, Appl
Sequence 20, Appl
Sequence 20, Appl
Sequence 27, Appl
Sequence 16, Appl
Sequence 16, Appl
Sequence 16, Appl
Sequence 17, Appl
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Sequence 315, App
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                                                                                                                                                                                                                                 September 22, 2004, 06:52:17; Search time 64 Seconds (without alignments) 10.631 Million cell updates/sec
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Sequence 10,
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1. /cgn2_6/ptodata/1/paa/USO6_NEW_COMB.pep:*

2. /cgn2_6/ptodata/1/paa/USO6_NEW_COMB.pep:*

3. /cgn2_6/ptodata/1/paa/USO8_NEW_COMB.pep:*

3. /cgn2_6/ptodata/1/paa/USO8_NEW_COMB.pep:*

3. /cgn2_6/ptodata/1/paa/USO8_NEW_COMB.pep:*

3. /cgn2_6/ptodata/1/paa/USO8_NEW_COMB.pep:*

3. /cgn2_6/ptodata/1/paa/USO8_NEW_COMB.pep:*

3. /cgn2_6/ptodata/1/paa/USO8_NEW_COMB.pep:*
                                GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-791-524A-124
US-10-342-081-76
US-10-729-156-4
US-10-877-930-33
US-10-977-930-20
US-10-912-764-34
US-10-912-764-34
US-10-912-764-34
US-10-912-764-34
US-10-912-764-34
US-10-808-758-78
US-10-808-758-78
US-10-808-758-78
US-10-808-758-78
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US-10-627-649-315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                       OM protein - protein search, using sw model
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Maximum DB seq length: 200000000
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Match Length
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1 CRGDC 5
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Perfect score:
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Sequence 148 Application US/09791524A
Sequence 148 Application US/09791524A
Sequence 148 Application US/09791524A

APPLICANT: Aventis Pharmaceuticals Products Inc.
TITLE OF INVENTION: Targeted Adenovirus Vectors For Delivery Of Heterologous Genes
FILE REFERENCE: P26, 992-B USA
CURRENT APPLICATION NUMBER: US/09/791,524A
CURRENT FILING DATE: 2001-02-22
PRIOR APPLICATION NUMBER: US 60/098,028
PRIOR PILING DATE: 1998-08-27
PRIOR FILING DATE: 1998-08-27
PRIOR FILING DATE: 1998-08-27
NUMBER OF SEQ ID NOS: 165
SOFTWARE: PatentIn version 3.2
SEQ ID NO 148
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                                 281, App
283, App
301, App
311, App
312, App
312, App
313, App
313, App
50090, A
336322,
336322,
20, App
21051,
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| Sequence 7, Application PC/TUS0416382
| GENERAL INFORMATION:
| APPLICANT: WEBER, Thomas
| APPLICANT: WEBER, Thomas
| APPLICANT: GIGOUT, Laure
| TITLE OF INVENTION: VIRAL VECTORS WITH IMPROVED PROPERTIES
| FILE REFERENCE: 02420/20M817-W00
| CURRENT APPLICATION NUMBER: PCT/US04/16382
| CURRENT PLLING DATE: 2004-06-01
| NUMBER OF SEQ ID NOS: 17
| SEQ ID NO 7
| LENGTH: 9
| LENGTH: 9
| TYPE: PRT | OTHER INFORMATION: peptide ligand
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Sequence
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                                              US-10-627-649-283
US-10-627-649-301
US-10-627-649-301
US-10-627-649-311
US-10-627-649-312
US-10-627-649-313
US-10-627-649-313
US-10-627-649-313
US-10-627-649-313
US-10-425-115-336324
US-10-808-758-20
US-10-808-758-2
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100.0%; Pred. No. 6.5e+05;
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US-10-808-758-16
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Best Local Similarity 100.
Matches 5; Conservative
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Cyclic Cell Adhesion Modulation Compounds
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CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/961,889
FILING DATE: 04-JUN-1993
APPLICATION NUMBER: US 07/550,330
FILING DATE: 09-JUL-1990
ATTORNEY AGENT INFORMATION:
NAME: BOSTICH, JUNE M.
REGISTRATION NUMBER: 31,238
REFERENCE/DOCKET NUMBER: Tanabe #7126/PD1381
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.25
GURENT APPLICATION DATA:
APPLICATION TOWNER: US/08/575,461
TITLE OF INVENTION: Cyclic Cell Adhesion Modul
TITLE OF INVENTION: Compounds
NUMBER OF SEQUENCES: 223
CORRESPONDENCES: 223
ADDRESSER: Spenaley Horn Jubas & Lubitz
STREET: 1880 Century Park East, Fifth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: 1
OTHER INFORMATION: /note= "Residue 1 is
OTHER INFORMATION: 1-adamantaneacetic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: Disulfide-bond;
LOCATION: 2..6
US-08-575-461-92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 9
SEQUENCE CHARATTERISTICS:
LENGTH: 6 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: Modified-site
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TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                         CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
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Best Local Similarity
Matches 5; Conserve
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                                                                                                                                                               Sequence 92, Application US/07961889
GENERAL INFORMATION:
APPLICANT: Lobi, Thomas J.
APPLICANT: Chiang, Shiu-Lan
APPLICANT: Cardarelli, Pina M.
TITLE OF INVENTION: Cyclic Cell Adhesion Modulation
TITLE OF SEQUENCES: 223
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: BM PC compatible
OPERATING SYSTEM: PC-COMPATIBLE
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/961,889
FILING DATE: 04-JUN-1993
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/550,330
FILING DATE: 09-JUL-1990
ATORNEY/AGENT INFORMATION:
NAME: BOSTICH, JUNE M.
REGISTRATION NUMBER: 31,238
REFERRNCE/DOCKET NUMBER: 31,238
REFERRNCE/DOCKET NUMBER: 31,238
REFERRNCE/DOCKET NUMBER: 31,238
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100.0%; Score 35; DB 3; 1
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 5; Conservative 0; Mismatches 0;
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OTHER INFORMATION: /note= "Residue 1 is
OTHER INFORMATION: 1-adamantaneacetic acid."
                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East, Fifth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
TELEPAK: (619) 455-5100
INPORMATION FOR SEQ ID NO: 92:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ) NAME/KEY: Disulfide-bond i LOCATION: 2..6 US-07-961-889-92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 6 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Los Angeles
STATE: California
                                                                                                                                                US-07-961-889-92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
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Gaps
                                        0; Indels
100.0%; Score 35; DB 9; 3 100.0%; Pred. No. 5.5e+06; Live 0; Mismatches 0;
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RESULT 15
US-08-575-461-92
; Sequence 92, Application US/08575461
; GENERAL INFORMATION:
; APPLICANT: Lobl, Thomas J.
; APPLICANT: Chiang, Shiu-Lan
; APPLICANT: Cardarelli, Pina M.

CRGDC 6

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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 35; DB 33; Length 5; 100.0%; Pred. No. 5.5e+06;
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100.0%; Score 35; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                    APPLICANT: Realvink, Petrus W
APPLICANT: Einfeld, David
APPLICANT: Einfeld, David
APPLICANT: Brough, Douglas E
APPLICANT: Lizonova, Alena
TITLE OF INVENTION: ALTERNATIVELY TARGETED ADENOVIRUS
FILE REFERENCE: 205046
CURRENT APPLICATION NUMBER: US/60/208,451
CURRENT FILING DATE: 2000-05-31
NUMBER OF SEQ ID NOS: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 7, Application PC/TUS9413542
GENERAL INFORMATION:
APPLICANT: La Jolla Cancer Research Foundation
TITLE OF INVENTION: Novel Integrin-Binding Peptides
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IEM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/13542

FILING DATE: 22-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRICE APPLICATION DATA:
APPLICATION NUMBER: US 08/158,001
FILING DATE: 24-00V-1993
ATTORNEY/AGENT INFORMATION:
NAME: HOOK, Gregory
REGISTARTION NUMBER: B8,701
REFERENCE/DOCKET NUMBER: FP-LA 1220
TELEPHONE: (619) 535-9001
Sequence 2, Application US/60208451
                                                  Wickham, Thomas J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                    Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : 6 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
CRGANISM: Homo sapiens
US-60-208-451-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: San Diego
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CRGDC 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PCT-US94-13542-7
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SEQ ID NO 2
LENGTH: 5
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APPLICANT: KOVESDI, INRE
APPLICANT: ROELVINK, PETRUS W
APPLICANT: BINFELD, DAVID
APPLICANT: BINFELD, DAVID
APPLICANT: BINFELD, DAVID
APPLICANT: LIZONOVA, ALENA
TITLE OF INVENTION NETHOD AND COMPOSITION FOR TARGETING AN ADENOVIRAL VECTOR
FILE REFERENCE: 220148
CURRENT APPLICATION NUMBER: US/10/304,160
CURRENT FILING DATE: 2001-05-30
PRIOR PLING DATE: 2001-05-30
PRIOR PLING DATE: 2000-08-09
PRIOR APPLICATION NUMBER: US 60/208451
PRIOR PLING DATE: 2000-08-09
PRIOR PLING DATE: 2000-08-31
SOFTWARE: PATENTING DATE: 2000-08-31
SOFTWARE: PATENTIN VET: 3.1
                                   APPLICANT: UNGER, EVAN C.
APPLICANT: UNGER, EVAN C.
APPLICANT: UNGER, EVAN C.
APPLICANT: MATSUNAGA, TERRY ONICHI
APPLICANT: RAMASKMAI, VARABARAJAN
APPLICANT: ROMANOWSKI, MAREK J.
TITLE OF INVENTION: NOVEL TARGETED DELIVERY SYSTEMS FOR BIOACTIVE AGENTS
FILE REFERENCE: 5030-0001.24
CURRENT APPLICATION NUMBER: US/09/912,609
CURRENT APPLICATION NUMBER: 09/703,474
PRIOR FILING DATE: 2000-10-7.25
PRIOR FILING DATE: 2000-01-05
PRIOR FILING DATE: 2000-01-05
PRIOR FILING DATE: 2000-01-05
NUMBER: OF SEQ ID NOS: 131
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Description of Artificial Sequence: Synthetic in OTHER INFORMATION: peptide US-09-912-609-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ô
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.0%; Score 35; DB 24; Length 5; Best Local Similarity 100.0%; Pred. No. 5.5e+06; Matches 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 35;
100.0%; Pred. No. !
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/10304160 GENERAL INFORMATION:
     Application US/09912609
                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
CORGANISM: Homo sapiens
US-10-304-160-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CRGDC 5
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RESULT 12 US-60-208-451-2

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APPLICANT: Unger. Evan C.

APPLICANT: Unger. Evan C.

APPLICANT: Unger. Beang
APPLICANT: Wu, Guanli
TITLE OF INVENTION: NOVel Targeted Compositions For Diagostics And Therapeutic Use
FILE REFERENCE: UNGRL598
CURRENT APPLICATION NUMBER: US/09/699,679A
CURRENT APPLICATION NUMBER: US/09/699,679A
FILING DATE: 1998-12-22
PRIOR PILING DATE: 1998-12-22
PRIOR APPLICATION NUMBER: 08/660,032
PRIOR PILING DATE: 1996-05-06
PRIOR PILING DATE: 1996-05-01
PRIOR APPLICATION NUMBER: 08/640,464
PRIOR APPLICATION NUMBER: 08/640,464
PRIOR APPLICATION NUMBER: 08/49,684
PRIOR APPLICATION NUMBER: 08/49,684
PRIOR PILING DATE: 1995-06-07

NUMBER OF SEQ ID NOS: 24

SEQ ID NO 24

LENGTH: 5

LENGTH: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 5;
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SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/627,035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
100.0%; Score 35; DB 20;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 5; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 35; DB 20; 100.0%; Pred. No. 5.5e+06;
                                                                                                                                                                                                              NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LA 9861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: both

sequence description: SEQ ID NO: 10:
US-09-627-035-10
                                                                 PILING DATE: 27-511-2000
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/212,186
FILING DATE: «Unknown»
ATTORNEY/ASETY INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Synthetic construct US-09-699-679A-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 24, Application US/09699679A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION TELEPHONE: (619) 535-900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ..
                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 5 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
PEATURE:
                                                                                                                                                                                                                                                                                                    TELEPHONE: (619) 533-1
TELEFAX: (619) 535-1
INFORMATION FOR SEQ ID NO: 10
                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Koivunen, Erkki
TITLE OF INVENTION: NOVEL INTEGRIN-BINDING PEPTIDES
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS: ADDRESSE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                           WEDION TYPE: REPORT disk
COMPUTER: IBM PC compatible
COURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/364,597A
FILING DATE: 30-01L-1999
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/158,001
FILING DATE: 24-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,861
FILING DATE: 04-ANG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn
NAME: Campbell, Cathryn
REGISTRATION NUMBER: 31,915
REGISTRATION NUMBER: 31,915
REGISTRATION NUMBER: 31,915
                                                               Sequence 37, Application US/09364597A
GENERAL INFORMATION:
APPLICANT: Ruoslahti, Erkki
APPLICANT: Kovounen, Erkki
TITLE OF INVENTION: Novel Integrin-Binding Peptides
NUMBER OF SEQUENCES: 46
                                                                                                                                                                                                                   ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 35; DB 17;
100.0%; Pred. No. 5.5e+06;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LA 3419
TELECOMMUNICATION INFORMATION:
TELEPHONE: (858) 535-9001
TELEPHONE: (858) 535-8949
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 10, Application US/09627035
GENERAL INFORMATION:
APPLICANT: Ruoslahti, Erkki I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                              CORRESPONDENCE ADDRESS: ADDRESSEE: Campbell 6
                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ,
US-09-364-597A-37
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                                                                                                                                                                                                                                                                                                                                                         ZIP: 92122
                                                   US-09-364-597A-37
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US-09-627-035-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Markhand Jr., Francis S.
APPLICANT: Bush, Larry R.
APPLICANT: Swenson, Stephen
APPLICANT: Stephen
APPLICANT: Stephen
APPLICANT: Stephen
ANTITHROMBOTIC
TITLE OF INVENTION: ACTIVITY
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Diatide, Inc.
STREET: 9 Delta Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/982,981
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/982,781
FILING BAPLICATION:
RICHARD AND AND APPLICATION NUMBER: US/08/753,781
FILING DATE: 02-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: MCDANIels, Patricia A.
REGISTRATION NUMBER: 33,194
REFERENCE/ODCKET NUMBER: DITI 124.1
TELECHMONICATION INFORMATION:
TELECHMONICATION INFORMATION:
TELECHMONICATION INFORMATION:
TELECHMONICATION INFORMATION:
TELEFRAK: 603 437 8977
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100.0%; Pred. No. 5.5e+06;
iive 0; Mismatches 0;
                                                                                                                                                                                                                             100.0%; Score 35; DB 11; 100.0%; Pred. No. 5.5e+06;
                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 45, Application US/08982981 GENERAL INFORMATION:
                                                      INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
312 913 0001
                                                                                                                                                                                                            Query Match
Best Local Similarity 100.
....nes 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.
Best Local Similarity 100.
Matches 5; Conservative
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                 TELEFAX: 312 913 0002
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MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 03053
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Londonderry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ČŘĠĎČ 5
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  TELEPHONE:
                                                                                                                                                                                      US-08-753-781B-45
                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-982-981-45
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SEQUENCE INFORMATION:

APPLICANT: Markland, Francis S
APPLICANT: Bush, Larry R
APPLICANT: Swenson, Stephen
TITLE OF INVENTION: Properties
NUMBER OF SEQUENCES: 54
CORRESPONDENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
STATE: Illinois
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                   FITLE OF INVENTION: NOVEL INTEGRIN-BINDING PEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CALF: COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
OPRENTIG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
#PPLICATION NUMBER: US/08/753,781B
FILING DATE: 02-DEC-1996
CLASSIFICATION: 435
                                                    ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 35; DB 10; 100.0%; Pred. No. 5.5e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 96
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Noonan, Kevin E
REGISTRATION NUMBER: 35,3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5; Conservative
                   NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CRGDC 5
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US-08-753-781B-45
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Gaps
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                     Length 5;
                                                                                                                                                                                                                                                                           APPLICANT: LIFORNATION:
APPLICANT: Lob1, Thomas J.
APPLICANT: Chiang, Shiu-Lan
APPLICANT: Cardarelli, Pina M.
TITLE OF INVENTION: Cyclic Cell Adhesion Modulation
TITLE OF INVENTION: Compounds
COMPRES OF SEQUENCES: 223
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRAILING SISIEM: Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/575,461
FILING DATE:
CLASSIFICATION TATA:
APPLICATION NUMBER: US/08/575,461
FILING DATE: US/08/575,461
APPLICATION NUMBER: US/07/550,330
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 35; DB 9;
100.0%; Pred. No. 5.5e+06;
                   100.0%; Score 35; DB 3; 1
100.0%; Pred. No. 5.5e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tanabe #7126/PD1381
                                                                                                                                                                                                                                                                                                                                                                                                                                      E: Spensley Horn Jubas & Lubitz
1880 Century Park East, Fifth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-625-695-10; Sequence 10, Application US/08625695; GENERAL INFORMATION:
                                                                                                                                                                                                                                      Sequence 55, Application US/08575461
GENERAL INFORMATION:
                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Bostich, June M.
REGISTRATION NUMBER: 31,238
REFERENCE/DOCKET NUMBER: Ta
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: Disulfide-bond LOCATION: 1..5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Ruoslahti, Erkk
APPLICANT: Koivunen, Erkki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (619) 455-5110 INFORMATION FOR SEQ ID NO: 5 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100...
Post Local Similarity 500...
                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 1880 CITY: LOS Angeles CITY: LOS Angeles CATATE: California COUNTRY: U.S.A.
7IP: 90067
Query Match
Best Local Similarity
''^a 5; Conserv?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CRGDC 5
                                                                                                       1 CRGDC 5
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US-08-575-461-55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 55, Application US/07961889
GENERAL INFORMATION:
APPLICANT: Lobl, Thomas J.
APPLICANT: Cardarelli, Pina M.
TITLE OF INVENTION: Cyclic Cell Adhesion Modulation
TITLE OF INVENTION: Compounds
NUMBER OF SEQUENCES: 223
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Jubas & Lubitz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/961,889
FILING DATE: 04.UUN-1993
CLASSIFTCATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tanabe #7126/PD1381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East, Fifth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 04-UN-1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/550,330
FILING DATE: 09-UL-1990
ATTORNEY/AGENI INFORMATION:
NAME: BOSILCh, UND M.
REGISTRATION NUMBER: 31,238
REFERNCE/DOCKET NUMBER: Tanabe #712
TELECOMMUNICATION INFORMATION:
                                                                                                                        REGISTRATION NUMBER: 38,701
REFERENCE/DOCKET NUMBER: FP-LA 1220
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: California
COUNTRY: U.S.A.
ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS
OPERATING SYSTEM: PC-DOS
                                      APPLICATION NUMBER: US 08/158,001
FILING DATE: 24-NOV-1993
ATTONEY/AGENT INFORMATION:
NAME: HOOK, GREGOTY
REGISTRATION NUMBER: 38,701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; FEATURE:
NAME/KEY: Disulfide-bond
; LOCATION: 1..5
US-07-961-889-55
                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 amino acids
                         PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                           , TIPE: amino acid ; TOPOLOGY: circular PCT-US94-13542-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Los Angeles
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CRGDC 5
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US-07-961-889-55
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Scoring table:

Searched:

protein

Run on:

Minimum I Maximum I

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Database

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Sequence 2, Appli
Sequence 7, Appli
Sequence 92, Appl
Sequence 92, Appl
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Sequence 10,
Sequence 45,
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Sequence 9, P
Sequence 2, P
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Sequence 37,
Sequence 10,
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Sequence 1
Sequence 1
Sequence 1
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Sequence
Sequence
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Sequence
Sequence
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Sequence
Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 37, Application PC/TUS9413542
Sequence 37, Application PC/TUS9413542
APPLICANT: La Jolla Cancer Research Foundation
TITLE OF INVENTION: Novel Integrin-Binding Peptides
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDLIUM TYPE: Floppy disk

COMPUTER: ELM C compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/13542

FILING DATE: 22-NOV-1994
                                       US-08-575-461-55

US-08-575-461-55

US-08-625-695-10

US-08-625-695-10

US-08-982-981-45

US-09-591-60-2

US-09-627-605-14

US-09-627-605-14

US-09-627-605-14

US-09-912-609-9

US-09-912-609-9

US-09-912-609-9

US-09-912-609-13

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US-09-91-13-91-13

US-09-91-13-13

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: San Diego
STATE: California
COUNTRY: USA
PCT-US94-13542-37
                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                        September 22, 2004, 06:49:42; Search time 430 Seconds (without alignments) 11.349 Million cell updates/sec
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19: /cgm2 6/ptodata/2/paa/USOB CONB.pep:*

10: /cgm2 6/ptodata/2/paa/USOB CONB.pep:*
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                      GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                 - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                               Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq length: 0
seq length: 200000000
                                                                                                                                                                                                                                                    US-09-912-609-9
35
1 CRGDC 5
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Match Length DB
                                            Copyright
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Perfect score:
Sequence:
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Score

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                                                                                   Query Match 100.0%; Score 35; DB 9; Length 9; Best Local Similarity 100.0%; Pred. No. 1.2e+06; Matches 5; Conservative 0; Mismatches 0; Indels
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Search completed: September 22, 2004, 07:06:15 Job time: 128 secs

1 CRGDC 5 ||||| 3 CRGDC 7

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Sequence 18, Application US/09164597A
Patent No. US20020103130A1
APPLICANT: Ruoslahti, Erkki
APPLICANT: Roslahti, Erkki
APPLICANT: No. US20020103130Alel Integrin-Binding Peptides
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
STREET: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 9;
            COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Patentin Release #1.0, Version #1.25
COSTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/364,597A
FLING DATE: 30-JUL-1999
CLASSIPICATION: 514
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/158,001
FILING DATE: 24-NOV-1993
FRIOR APPLICATION NUMBER: US 08/286,861
FILING DATE: 04-AGG-1994
ATTORNEY AGENT INFORMATION:
REGISTRATION NUMBER: 31.815
REFERENCE JOOKET NUMBER: P-LA 3419
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (858) 535-9001
TELEPHONE: (858) 535-9001
TELEPHONE: GRANGTERISTICS:
SEQUENCE CHARACTERISTICS:
LEMATH. O SMITCH CONTINENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MDIUM TRY:
MDIUM TRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 35; DB 9; 100.0%; Pred. No. 1.2e+06;
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REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-1
TELECOMMUNICATION INFORMATION:
Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match
Best Local Similarity 100.
Matches 5, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            i LENGTH: 9 amino acida;
TYPE: amino acid
i TOPOLOGY: circular
US-09-364-597A-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -09-364-597A-18
                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Rolabalt, Erkti
APPLICANT: Rolabalt, Erkti
APPLICANT: Rolabalt, Erkti
APPLICANT: Rolabalt Erkti
MUMBER OF INVENTION: No. US20020103130A1e1 Integrin-Binding Peptides
CORRESPONDENCE ST.
STADESSEE: Campbell & Flores LLP
STREET: California
CUITY: San Diego
CONFORTS: Galfornia
COMPUTES: Band A
COMPUTES: Band PC Compatible
COMPUTES: Band PC Compatible
OPERATING SYSTEM: PC-PONNS-LDS
SOFTWARE: Patentin Release #1.0, Version #1.25
APPLICATION NOMBER: US/09/364,597A
FILING DATE: 30-JUL-1999
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/158,001
FILING DATE: 24-NOV-1993
APPLICATION NUMBER: US 08/158,001
FILING DATE: Cambbalt, Cathryn
NAME: Cambbalt, Cathryn
RESISTAATION NUMBER: 13,815
RESISTAATION POR SEO ID NO: 16:
TELEFAX: (688) 535-9001
TELEFAX: G889 335-9001
TELEFAX: G889 31-815
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**Patent No. US20020103130A1

GENERAL INPOMENTION:

APPLICANT: Ruoslahti, Erkki

APPLICANT: Koivunen, Erkki

APPLICANT: Sounbenli & Flores Lip

STREET: 4170 La Jolla Village Drive, Suite 700

STREET: Galifornia

CITY: San Diego

STATE: Galifornia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
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                                                                                            Sequence 16, Application US/09364597A Patent No. US20020103130A1 GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 5; Conservative
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COMPUTER READABLE FORM:
                                                          US-09-364-597A-16
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US-09-364-597A-17
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Query Match
Best Local Similarity 100.
Matches 5; Conservative
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CITY: San Diego
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 5; Conserv
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TOPOLOGY:
US-09-364-597A-15
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APPLICANT: Krasnykh, Victor N.
APPLICANT: Dmitriev, Igor
TITLE OF INVENTION: Adenovirus Vector Containing A Heterologous Peptide
TITLE OF INVENTION: Epitope in the HI Loop of the Fiber Knob
TITLE OF INVENTION: BOSOO
CURRENT APPLICATION NUMBER: US/09/245,603A
CURRENT APPLICATION 1999-02-05
                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Description of Artificial Sequence: RGD-4C peptide
                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 35; DB 9; Length 9; Best Local Similarity 100.0%; Pred. No. 1.2e+06; Matches 5; Conservative 0; Mismatches 0; Indels
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TITLE OF INVENTION: Chimeric Prostate-Homing Peptides With TITLE OF INVENTION: Pro-Apoptotic Activity FILE REFERENCE: P-LJ 3844
CURRENT APPLICATION NUMBER: US/09/765,086
CURRENT FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: US 09/489,582
PRIOR PILING DATE: 2000-01-1
NUMBER OF SEQ ID NOS: 235
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: HAYARAWA, TAKAO
TITLE OF INVENTION: ADENOVIRUS VECTOR
FILE REFERENCE: 081365/016
CURRENT APPLICATION NUMBER: US/09/845,160
CURRENT FILING DATE: 2001-05-01
PRIOR APPLICATION NUMBER: JP 2001-131688
PRIOR PELING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: JP 2000-161577
PRIOR PILING DATE: 2000-05-31
                                                                                                                                                                                                                                                                                       FEATURE:
; OTHER INFORMATION: synthetic peptide
US-09-765-086-1
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Patent No. US20020081280A1
GENERAL INFORMATION:
APPLICANT: Curiel, David T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5, Application US/09845160
Patent No. US20020058045A1
GENERAL INFORMATION:
APPLICANT: MIZUGUCHI, HIROYUKI
                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 5
LENGTH: 9
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US-09-245-603A-16
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US-09-845-160-5
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PRIOR APPLICATION NUMBER: US 60/099,801
PRIOR FILING DATE: 1998-09-10
NUMBER OF SEQ ID NOS: 17
SEQ ID NO 16
LENGTH: 9
TYPE: PRT
OTHER INFORMATION: Amino acid sequence of a RGD peptide incorporated
OTHER INFORMATION: into the region of the fiber gene within the HI loop.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Ruoslahti, Erkki
APPLICANT: Rosunen, Erkki
TITLE OF INVENTION: No. US20020103130Alel Integrin-Binding Peptides
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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100.0%; Pred. No. 1.2e+06;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                     0; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 30-JUL-1999
CLASSIFICATION 314
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/158,001
FILING DATE: 24-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,861
FILING DATE: 04-NOV-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                       100.0%; Score 35; DB 9; I
100.0%; Pred. No. 1.2e+06;
                                                                                                                                                                                                                                                                                                                                        0; Mismatches
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (858) 535-9001
TELEFAX: (858) 535-8949
INFORMATION FOR SEQ ID NO: 15:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 15, Application US/09364597A Patent No. US20020103130A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Campbell, Cathryn REGISTRATION NUMBER: 31,815
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Sequence 148, Application US/09791524
Publication No. US20030143209A1
GENERAL INFORMATION:
APPLICANT: Aventis Pharmaceuticals Products Inc.
TITLE OF INVENTION: Targeted Adenovirus Vectors For Delivery Of Heterologous Genes TITLE OF INVENTION: Targeted Adenovirus Vectors For Delivery Of Heterologous Genes CURRENT APPLICATION NUMBER: US/09/791,524
CURRENT APPLICATION NUMBER: 60/09828
PRIOR PILING DATE: 1998-08-27
NUMBER OF SEQ ID NOS: 150
SOFTWARE: Patentin version 3.0
ELENTING 148
ELENTING ARE ADELICATION USE ADELICATION 
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ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Adenovirus
US-09-791-524-148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 5; Conserv
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                                                       RESULT 7
US-09-791-524-148
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                               Sequence 10, Application US/09912609
FUBLICATION NO. US20020041898A1
GENERAL INFORMATION:
APPLICANT: UNGER, EVAN C.
APPLICANT: WATSUNAGA, TERY ONICHI
APPLICANT: RAMASWAMI, VARBARAANA
TITLE OF INVENTION: NOVEL TARGETED DELIVERY SYSTEMS FOR BIOACTIVE AGENTS
TITLE OF INVENTION: NOVEL TARGETED DELIVERY SYSTEMS FOR BIOACTIVE AGENTS
CURRENT APPLICATION NUMBER: US/09/912,609
FILE REFERENCE: 5001-07-25
PRIOR APPLICATION NUMBER: 09/703,474
PRIOR APPLICATION NUMBER: 09/703,474
PRIOR PELING DATE: 2000-10-31
PRIOR PELING DATE: 2000-10-31
PRIOR PELING DATE: 2000-10-31
SPIOR FILING DATE: 2000-10-13
SOFTWARE: PALENT NUMBER: 09/478,124
NUMBER OF SEQ ID NOS: 131
SEQ ID NOS: 131
SEQ ID NO S: 121
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APPLICANT: UNGER EVAN C.
APPLICANT: WASSUNAGA, TERRY ONICHI
APPLICANT: RAMASWAMI, VARADARAJAN
TITLE OF INVENTION: NOVEL TRRETE J.
TITLE OF INVENTION: NOVEL TRRETED DELIVERY SYSTEMS FOR BIOACTIVE AGENTS
FILE REFERENCE: 5030-0001.24
CURRENT FILING DATE: 2001-07-25
PRIOR PELICATION NUMBER: 09/703,474
PRIOR PELICATION NUMBER: 09/478,124
PRIOR PELICATION NUMBER: 09/478,124
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 131
SOFTWARE: PATENTIN VET. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Description of Artificial Sequence: Synthetic US-09-912-609-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
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100.0%; Score 35; DB 12; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.20+06;
Matches 5; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Score 35; DB 12; Length 6;
Matches 5; Conservative 0; Mismatches 0; Indels
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Sequence 13, Application US/09912609

Publication No. US20020041898A1

GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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US-09-912-609-10
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Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Synthetic amino acid sequence US-10-013-009-4
                                                                   APPLICANT: McMorris, Trevor C.
APPLICANT: Kelner, Michael J.
TITLE OF INVENTION: Antitumor agents
FILE REPERBNCE: 103.008033
CURRENT APPLICATION NUMBER: US/10/013,009
CURRENT FILING DATE: 2001-11-05
PRIOR APPLICATION NUMBER: US 09/386,555
PRIOR PILING DATE: 1999-08-11
PRIOR PLING DATE: 1998-02-20
PRIOR PLING DATE: 1998-02-20
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FRSESEQ for Windows Version 3.0
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/09765086; Patent No. US20010046498A1.
GENERAL INFORMATION: APPLICANT: Rucelahri, Erki
APPLICANT: Paequalini, Renata
APPLICANT: Wadlh, Arap
APPLICANT: Bredesen, Dale E.
Sequence 4, Application US/10013009
Publication No. US20020086815A1
GENERAL INFORMATION:
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Indels

100.0%; Score 35; DB 14; Length 5; 100.0%; Pred. No. 1.2e+06;

; Pred. No. 1.2e+06; 0; Mismatches 0;

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PRIOR FILING DATE: 2000-05-31
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin Ver. 3.1
SEQ ID NO 2
                                                                                                                                                                                  Query Match 100.
Best Local Similarity 100.
Matches 5; Conservative
                                                                              LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-304-160-2
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APPLICANT: ROUSDI, IMRE
APPLICANT: RINFELD, DAVID
APPLICANT: BINFELD, DAVID
APPLICANT: BINFELD, DAVID
APPLICANT: LIZONOVA, ALENA
TITLE OF INVENTION: METHOD AND COMPOSITION FOR TARGETING AN ADENOVIRAL VECTOR
FILE REPRENCE: 201048
CURRENT APPLICATION NUMBER: US/10/304,160
CURRENT PILING DATE: 2002-11-25
PRIOR APPLICATION NUMBER: PCT/US01/17391
PRIOR FILING DATE: 2000-08-09
                                                                                                                                                                                                                                                                                                                                                   Sequence 9, Application US/09912609

Sequence 9, Application US/09912609

Publication No. US20020041898A1

GENERAL INFORMATION:

APPLICANT: UNGER, EVAN C.

APPLICANT: MATSUNAGA, TERRY ONICHI

APPLICANT: RAMASWAMI, VARADARAJAN

APPLICANT: RAMASWAMI, VARADARAJAN

APPLICANT: RAMASWAMI, VARADARAJAN

APPLICANT: RAMASWAMI, VARADARAJAN

CURRENT: RAMASWAMI, VARADAREK J.

TILLE OF INVERTION: NOVEL TARGETED DELIVERY SYSTEMS FOR BIOACTIVE AGENTS

CURRENT APPLICATION NUMBER: US/09/912,609

CURRENT FILING DATE: 2000-10-31

PRIOR FILING DATE: 2000-10-31

PRIOR FILING DATE: 2000-10-10-5

NUMBER OF SEQ ID NOS: 131

SEQ ID NO 9

LENGTH: 5

LENGTH: 5

LENGTH: 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic; CTHER INFORMATION: peptide
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                                                                                                                         100.0%; Score 35; DB 9; Length 5; 100.0%; Pred. No. 1.2e+06; Mismarches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/10304160 Publication No. US20030099619A1 GENERAL INFORMATION: APPLICANT: WICKHAM, THOMAS J
      37:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
; INFORMATION FOR SEQ ID NO: 3
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: circular
US-09-364-597A-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.v.
-ham 5; Conservative
                                                                                                                      Query Match
Best Local Similarity 100.
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US-10-304-160-2
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                                                                               APPLICANT: Ruoslahti, Erkki
APPLICANT: Ruoslahti, Erkki
APPLICONT: Kolvunen, Brkki
TITLE OF INVENTION: No. US20020103130Alel Integrin-Binding Peptides
NUMBER OF SEQUENCES: 46
CORRESSONDEMESS: 6
CORRESSONDEMESS: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                            COMPUTER FEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floor Mark:
APPLICATION DATA:
APPLICATION NUMBER: US 08/158,001
FILING DATE: 24-NOV-1993
PRIOR APPLICATION NUMBER: US 08/286,861
FILING DATE: 04-AUG-1993
RILING DATE: 04-AUG-1994
ATPONEY/AGENT: INFORMATION:
AMPLICATION NUMBER: US 08/286,861
FILING DATE: 04-AUG-1994
ATPONEY/AGENT: INFORMATION:
AMPLICATION NUMBER: US 08/286,861
FILING DATE: 04-AUG-1994
ATPONEY/AGENT: INFORMATION:
AMPLICATION NUMBER: US 08/286,861
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100.0%; Pred. No. 1.2e+06;
tive 0; Mismatches 0;
Sequence 7, Application US/09364597A; Patent No. US20020103130A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Campbell, Cathryn
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LA
TELECOMMUNICATION INPORMATION:
TELEPHONE: (858) 535-9001
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                            CITY: San Diego
STATE: California
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Best Local Similarity
5; Conserve
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Sequence 5, Appli Sequence 3, Appli Sequence 4, Appli Sequence 14, Appl Sequence 22, Appl Sequence 38, Appl Sequence 62, Appl Sequence 63, Appl Sequence 63, Appl

Sequence 2, Appl. Sequence 124, Appl. Sequence 419, Appl. Sequence 451, Appl. Sequence 451, Appl. Sequence 1076, Appl. Sequence 1076, Appl. Sequence 451, Appl. Sequence 451, Appl. Sequence 419, Appl. Sequen

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Sequence 37, Application US/09364597A

Sequence 37, Application US/09364597A

Patent No. US20020103130A1

GENERAL INFORMATION:

APPLICANT: Rucellaht, Erki

APPLICANT: Rucellaht, Erki

TITE OF INVENTION: No. US20020103130A1e1 Integrin-Binding Peptides

CORRESPONDENCE ADDRESS:

ADDRESSEE: Campbell & Flores LLP

STREET: 4370 La Jolla Village Drive, Suite 700

STATE: California

COUNTRY: USA

ITE: OS 122

COMPUTER READALLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/WS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

APPLICATION NUMBER: US/09/364,597A

CLASSTFICATION DATA:

APPLICATION NUMBER: US 08/158,001

FILING DATE: 30-JUL-1999

CLASSTFICATION DATE: US 08/286,861

FILING APPLICATION DATA:

APPLICATION NUMBER: US 08/286,861

FILING APPLICATION DATE:

APPLICATION NUMBER: US 08/286,861
           US-09-364-597A-33

US-09-734-628-1

US-09-971-798-5

US-09-969-192-4

US-09-840-277-14

US-09-840-277-22

US-09-840-277-23

US-09-840-277-38

US-09-840-277-62

US-09-840-277-62

US-09-840-277-62

US-09-840-277-63

US-09-840-277-63

US-09-810-277-63

US-10-609-217-455

US-10-609-217-455

US-10-609-217-455

US-10-609-217-1076

US-10-632-388-450

US-10-631-733-452

US-10-651-723-452

US-10-651-723-452

US-10-651-723-452
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REGISTRATION NUMBER: 31,015
REFERENCE/DOCKET NUMBER: P-LA 3419
TELECOMMUNICATION INFORMATION:
TELEPHONE: (858) 535-8041
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           Sequence 37, Appl Sequence 9, Appli Sequence 10, Appli Sequence 10, Appli Sequence 13, Appli Sequence 14, Appli Sequence 1, Appli Sequence 1, Appli Sequence 15, Appli Sequence 15, Appli Sequence 16, Appli Sequence 17, Appli Sequence 11, Appl
                                                                                                                                            September 22, 2004, 06:53:03; Search time 127 Seconds (without alignments) 12.643 Million cell updates/sec
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| Cgn2_6/ptodata/1/pubpaa/USO7 PUBCOMB.pep:*
| Cgn2_6/ptodata/1/pubpaa/PCT NEW PUB.pep:*
| Cgn2_6/ptodata/1/pubpaa/USO6 NEW PUB.pep:*
| Cgn2_6/ptodata/1/pubpaa/USO6 PUBGOMB.pep:*
| Cgn2_6/ptodata/1/pubpaa/USO7 NEW PUB.pep:*
| Cgn2_6/ptodata/1/pubpaa/USO7 NEW PUB.pep:*
| Cgn2_6/ptodata/1/pubpaa/USO8 NEW PUB.pep:*
| Cgn2_6/ptodata/1/pubpaa/USO8 PUBCOMB.pep:*
| Cgn2_6/ptodata/1/pubpaa/USO8 PUBCOMB.pep:*
| Cgn2_6/ptodata/1/pubpaa/USO8 PUBCOMB.pep:*
| Cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
| Cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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2 US-09-912-609-9
4 US-10-304-160-2
4 US-09-912-609-10
2 US-09-912-609-13
2 US-09-912-609-13
2 US-09-912-609-13
3 US-09-912-609-13
3 US-09-765-086-1
US-09-945-160-5
US-09-945-603A-16
US-09-364-597A-17
US-09-364-597A-17
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                                                                                        OM protein - protein search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Match Length DB
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Perfect score:
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A complex used for thrombus imaging comprises technetium-99m complexed with a peptide ligand for GPIIb/IIIa receptor.
                                                                                                                                                                                Thrombus imaging; fibrin polymerisation site; technetium-99m; Tc-99m; GPIIb/IIIa receptor; cyclic peptide ligand.
                                                                                                                                     Peptide ligand for fibrin polymerisation site.
  AAY54976 standard; peptide; 5 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                       92US-00886052.
94US-00273274.
                                                                                                                                                                                                                                                                                                                                                                                            95US-00484773.
                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dean RT, Lister-James J;
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nes 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                       21-MAY-1992;
11-JUL-1994;
                                                                                          15-FEB-2000
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                                                                                                                                                                                                                                                         Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to reagents (A) for preparing thrombus imaging agents comprising specific binding peptides (I) and a technetium-99m binding group (II) covalently attached to the specific binding peptide. (I) is a ligand for the GPIID/IIIa receptor and can be a cyclic or linear peptide not containing the Arg-Gly-Asp (RGD) sequence. (I) are specific for thrombi, and are small and therefore are rapidly cleared from blood and background tissue. (A) are used to produce scintigraphic imaging agents for detection of thrombi in vivo. The present sequence is one such TC-99m labelled peptide.
                                                                                                                                     Gaps
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                                                                                            Length 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thrombus imaging agent; GPIIb/IIIa receptor; thrombus.
                                                                                   100.0%; Score 35; DB 2; L
100.0%; Pred. No. 1.4e+06;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Reagent for preparing thrombus imaging agent.
                                                                                                                                                                                                                                                                                                                                             ADE25491 standard; peptide; 5 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91US-00653012.
91US-00807062.
92US-00886752.
94US-00264176.
94US-00273274.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95US-00478725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tc-99m labelled peptide #19
                                                                                                                                                                                                                                                                                                                                                                                                                                  29-JAN-2004 (first entry)
inexpensively synthesised
                                                                                   Query Match
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dean RT, Lister-James J;
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                                                                                                                                                                                CRGDC 5
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                                             Sequence 5 AA;
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                                                                                                                                                                                                                                                                                                                                                                                          ADE25491;
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                                                                                                                                                                                                                                                                                                  RESULT 14
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                                                                    This sequence represents a peptide ligand for the fibrin polymerisation site. The invention relates to a complex (A) for thrombus imaging comprises technetium-99m (Tc-99m) completed with a reagent comprising a peptide (P) with 4 to 100 amino acids sequence and a Tc-99m binding moiety covalently bound to (P). (P) is selected from a linear peptide ligand for a GPIIb/IIIa receptor not comprising the amino acid sequence (arginine-glycine-aspartate), a peptide ligand for a polymerisation site of fibrin, and a cyclic peptide ligand for the GPIIb/IIIa receptor. The thrombus imaging reagents provided by the present invention can be used for visualising thrombi in a mammalian body when Tc-99m is labelled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 35; DB 3; Length 5; 100.0%; Pred. No. 1.4e+06; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Search completed: September 22, 2004, 06:51:44 Job time : 124 secs
Example 2; Col 13-14; 18pp; English.
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Gaps

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Similarity 100.0%; Score 35; DB 2; Length 5; Similarity 100.0%; Pred. No. 1.4e+06; 5; Conservative 0; Mismatches 0; Indels

Query Match Best Local Similarity Matches 5; Conserv

1 CRGDC 5 ||||| 1 CRGDC 5

RESULT 15 AAY54976

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The invention relates to new thrombolytic agents which comprise a capable of specifically binding to a component of a thrombolytic proteinase covalently linked to a targetting compound thrombolytic agents can be used for eliminating thrombi in vivo in, myocardial infarction, cerebral ischaemia, deep vein thrombosis or pulmonary embolism. A labelled form of the thrombolytic agent can also be used to image thrombi for diagnostic purposes. The thrombolytic agents are specifically targetted to thrombus sites in vivo and have minimal hamaorrhagic side effects and side effects related to non specific proteclysis. The present sequence represents a specifically claimed targetting peptide. (Updated on 25-MAR-2003 to correct PI field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Reagent useful for preparing thrombus imaging agent - comprises peptide covalently linked to technetium binding moiety which is technetium labelled and binds to thrombus component.
                                                                                                New thrombolytic agents - comprise thrombolytic proteinase covalently linked to targetting compound for binding to component of thrombus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Technetium-99M label; thrombus imaging; GPIIb/IIIA receptor; ligand;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GPIIb/IIIa receptor ligand with technetium-99M binding moiety.
                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 35; DB 2; Length 5; 100.0%; Pred. No. 1.4e+06; tive 0; Mismatches 0; Indels
                                           Flores Sanchez E;
                                           Swenson S,
(DIAT-) DIATIDE INC.
(UYSC-) UNIV SOUTHERN CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW50594 standard; peptide; 5 AA.
                                                                                                                                             Claim 10; Page 65; 79pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91US-00653012.
91US-00807062.
92US-00886052.
94US-00264176.
94US-00273274.
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                                                                                                                                                                                                                                                                                                                                                                                                               5; Conservative
                                         Bush LR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1998-239148/21.
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                                                                      WPI; 1998-333336/29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   binding moiety
                                                                                                                                                                                                                                                                                                                                                       Sequence 5 AA;
                                         Markland FS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-MAY-1992;
22-JUN-1994;
11-JUL-1994;
07-JUN-1995;
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Gaps

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The invention relates to peptides having specific binding specificity for fibronectin-binding and vitronectin-binding integrins, and in particular for alphasberal integrin. The peptides can be used in a method of preventing integrin-mediated attachment to an extracellular matrix protein, fibronectin, or vitronectin which comprises (a) contacting the cells with a soluble peptide selected from the sequences shown in AAY21561, AAY21563 and AAY21586; or (b) contacting the sequence shown in AAY21561, and alpha the sequence -NGR- selected from the sequences soluble peptide comprising the sequence -NGR- selected from the sequences contacting with a soluble peptide shown in AAY21571. The peptides are useful for inhibiting metastatic process with which fibronectin adhesion is associated and also for inhibiting alpha v beta 1-mediated cell attachment to fibronectin, are also useful for promoting attachment to vitronectin. The peptides are also useful for promoting attachment to fibronectin. The peptides are also useful for promoting attachment to fibronectin.
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                             The invention relates to a reagent for preparing a thrombus imaging agent. It comparises: (a) a specific binding peptide (BP) having a sequence of 4-100 manio acids; and (b) a technetium-99m binding moiety (TBM) covalently linked to the peptide which binds to a component of a thrombus. TBM forms an electrically neutral complex with technetium-99m. The small size of the peptide component of the reagent enhances blood and background tissue clearance and it is easy to prepare. This sequence represents a GPID/IIIa receptor binding peptide covalently linked to a
                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Integrin; fibronectin; vitronectin; extracellular matrix protein; metastatic; fibronectin adhesion; alpha5betal integrin.
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                                                                                                                                                                                                                                                               Length 5;
                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                             100.0%; Score 35; DB 2; I 100.0%; Pred. No. 1.4e+06;
                                                                                                                                                                                                                                                                                                  Mismatches
Example 2; Col 11-12; 18pp; English.
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                                                                                                                                                                                     technetium-99m binding moiety
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94US-00212186.
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                                                                                                                                                                                                                                                                                                    Conservative
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Best Local Similarity
E.t. 5, Conserv?
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                                                                                                                                                                                                                           Sequence 5 AA;
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RESULT 9

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The present sequence represents a synthetic peptide which acts as an antendral antendral between the invention provides various antendral because they mimic extra-cellular matrix ligands or other cell adhesion ligands that bind to receptors such as integrin receptors, including fibronectin. Immin. LFA-1, MAC-1, p150, 95, vitronectin and gplib/lira receptors. Some of the peptides contain the amino acid sequence Arg-Gly-Asp (RGD). Others contain non-RGD sequences, for e.g RCD sequences, and reverse cuseful in modulating cell adhesion, including adhesion related to fibronectin, as well as leukocyte adhesion to endothelial cells. They are also claimed to be useful in the study, diagnosis, treatment or prevention of diseases which relate to cell adhesion, e.g. adult respiratory distress syndrome (ARDS), thrombosis and inflammatory conditions
                                                                                                                                                                                                                                                                                  New cyclic peptide(8) and peptidomimetic compounds - are integrin receptor antagonists useful in modulating cell adhesion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Targetting peptide #45 useful as component of thrombolytic agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thrombolytic agent; thrombolytic proteinase; blood clot; fibrin; thrombus; antithrombotic activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      / Match 100.0%; Score 35; DB 2; Length 5; Local Similarity 100.0%; Pred. No. 1.4e+06; les 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                   Chiang S;
                                                                                                                                                                                                                                                                                                                                    Example 9; Col 42; 32pp; English.
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                                                                                                                                91WO-US004862.
                                                                                 95US-00485019
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(first entry)
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                                                                                                                                                                                                                  Cardarelli PM,
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                                                                                                                                09-JUL-1991;
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23-SEP-1998
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                 US5721210-A
                                              24-FEB-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptides AAW03483-508 are examples of synthetic peptides generated to bind to the fibronectin/vitronectin-binding integrin alpha(5)beta(1). They are synthesised to contain the alpha(5)beta(1)-integrin peptide binding motifs: DGR, NGR or RGD. The peptides interfere with the binding of fibronectin and vitronectin to this integrin and thus may be used to block integrin-mediated cell adhesion to extracellular matrix proteins, esp. to inhibit tumour metastasis. (Updated on 25-MAR-2003 to correct PF
                                                                                                                                                                                           Synthetic; fibronectin; vitronectin; integrin; binding motif; adhesion; extracellular matrix protein; tumour metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic integrin-binding peptide(s) - useful for inhibiting tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Integrin receptor antagonist, cell adhesion modulator; leukocyte; extracellular matrix; fibronectin; ARDS; thrombosis; inflammation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 35; DB 2; Length 5; 100.0%; Pred. No. 1.4e+06; ive 0; Mismatches 0; Indels
                                                                                                                                                       Alpha(5)-Beta(1) integrin binding peptide 10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Integrin receptor antagonist peptide 38.
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Disulfide-bond 1..5
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                                         AAW03492 standard; peptide; 5 AA.
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                                                                                                                                                                                                                                                                                                                                               94US-00212186
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24-OCT-1996
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                                                                                                                                                                                         Synthetic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to reagents for scintigraphic imaging of a thrombus in-vivo, comprising (A) a specific binding compound capable of binding to at least one component of a thrombus, covalently linked to (B) a technetium-99m-binding moiety. Specific peptides constituting the reagents are claimed as new. The present peptide is one such peptide. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                       The peptide sequence is an example of a highly generic sequence contg. the RGD motif. Compounds contg. these lipid peptides are useful as cell migration inhibitors in cell adhesion membranes or cell culture bodies. See also AAR29048-54
                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gp IIb/IIIa receptor ligand used in scintigraphic imaging of thrombi
                                         New synthetic peptide lipids or salts - useful as cell migration inhibitors, cell adhesion membranes and cell culture bodies.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Scintigraphy, thrombus, thrombi, imaging, specific binding, technetium-99m, radiolabelled, Gp IIb/IIIa receptor ligand.
                                                                                                                                                                                                                  100.0%; Score 35; DB 2; Length 5; 100.0%; Pred. No. 1.4e+06; ive 0; Mismatches 0; Indels
                                                                                      Disclosure; Page 3; 9pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 41; Page 46; 61pp; English.
                                                                                                                                                                                                                                                                                                                                                                                    AAR69325 standard; peptide; 5 AA
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25-JUN-1995
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The sequences given in AAR76185-200 and AAR79073-94 are high affinity integrin binding peptides which bind to various integrins. Peptides which bind to alphas/betal integrins contain the motifs given in AAR76185-86 and peptides which bind to alphas/beta5 and alphas/beta3 integrins are also contain the motif given in AAR76187. Alphav/beta5 integrins are also contain the motif given in AAR76187. Alphav/beta5 integrins are also conformationally stabilised configuration which is due to the formation of a disulphide bond, a peptides of a dactam bond. These peptides may be used for isolating the complementary integrin from a sample mixture by contacting them under ionic conditions to allow binding of the integrin to the peptide and then separating the integrin from the peptide and then separating the integrin from the peptide. They can be used for attaching cells to a substrate, by binding them to the substrate with the cell. The peptides promote wound healing when applied locally and inhibit the attachment of osteoclasts to bone. They inhibit angiogenesis, metastasis of tumours and migration of smooth muscle cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            High affinity integrin binding peptides - can be used to attach cells to a substrate, inhibit the attachment of osteoclasts to bone, promote wound healing, inhibit angiogenesis, metastasis of tumours and migration of smooth muscle cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                     High affinity; integrin binding peptide; alphas/betal; alphav/beta5; alphav/beta3; RGD; stable configuration; wound healing; osteoclast attachemnt; bone; angiogenesis; metastasis; tumour; smooth muscle cell migration.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 35; DB 2; I 100.0%; Pred. No. 1.4e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                         Alpha5/betal integrin binding peptide #20.
                                                                                                                                                                                                                                                                                                  Location/Qualifiers 1. .5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (LJOL-) LA JOLLA CANCER RES FOUND.
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                                 AAR79093 standard; peptide; 5 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93US-00158001.
94US-00286861.
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                                                                                                      (first entry)
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                       Disulfide-bond
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                                                                                                                                                                                                                                                                                                                                                                                                                               22-NOV-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ruoslahti E,
                                                                                                        24-JAN-1996
                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-1995
                                                                                                                                                                                                                                                                   Synthetic
                                                                    AAR79093;
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Matches
RESULT 8
                  AAR79093
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Gaps

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100.0%; Score 35; DB 2; Length 5; 100.0%; Pred. No. 1.4e+06; cive 0; Mismatches 0; Indels

Conservative

Local Similarity

Matches

Query Match

cell culture body.

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To residue homoCys1 is attached Acetyl and to residue Cys5 is attached

NH2. The peptide is prepd. using standard methods of solid phase

the synthesis and is one of 17 pref. examples of a highly generic formula.

The peptide is used to inhibit fibrinosen-induced platelet aggregation

and is partic. useful because it does not significantly deplete the

platelet count. It has a relatively short duration of activity and is

thus useful where prevention of platelet aggregation over a short period

of time is desirable, e.g. in surgery of peripheral arteries and

cardiovascular surgery. It is also useful in prevention of platelet

thrombosis, thromboembolism and reocclusion either during and after

thrombolytic therapy, or after angioplasty of coronary and other arteries

thrombolytic therapy, or after angioplasty of coronary and other arteries

chrombolytic therapy, or after angioplasty of coronary and other arteries

thrombolytic therapy, or after of thrombolytic agents, e.g. plasminogen

activators or streptokinase, or anticoagulants. See also AAR10413-18 and

EP-410537, EP-410539, EP-410540, EP-410541, and EP-410767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New fibrinogen receptor antagonising peptide cpds. - used to inhibit
blood platelet aggregation during surgery on peripheral arteries and in
cardiovascular surgery.
                                                                                 Fibrinogen receptor antagonist, platelet aggregation; thrombosis; myocardial infarction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic; cell migration; inhibitor; cell adhesion membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 35; DB 2; Length 5; 100.0%; Pred. No. 1.4e+06; ive 0; Mismatches 0; Indels
                                              Fibrinogen receptor antagonising peptide (VI).
                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR27031 standard; peptide; 5 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 7; Page 10; 10pp; English.
                                                                                                                                                                                                      1. .1
/label= homoCys
                                                                                                                                                                                                                                                                                                                                                                                                                 Veber DF;
                                                                                                                                                                                                                                                                                                                 90EP-00202015
                                                                                                                                                                                                                                                                                                                                                 89US-00386534
                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1991-030928/05.
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es 5; Conserv
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                                                                                                                                                                              Disulfide-bond
Modified-site
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                                                                                                                                                                                                                                                                                                             23-JUL-1990;
                                                                                                                                                                                                                                                                                                                                              28-JUL-1989;
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                                                                                                                                                                                                                                                 EP410537-A
                                                                                                                                 Synthetic.
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Gaps

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The peptide sequence is an example of a highly generic sequence contg. the RGD motif. Compounds contg. these lipid peptides are useful as cell migration inhibitors in cell adhesion membranes or cell culture bodies. See also AAR27027-33
                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                        New synthetic peptide lipid(s) and salts - useful as cell migration inhibitors, cell adhesion membranes or cell culture bodies.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic; cell migration; inhibitor; cell adhesion membrane; cell culture body.
                                                                                                                                                                                                                                                                                                                         100.0%; Score 35; DB 2; Length 5; 100.0%; Pred. No. 1.4e+06; ive 0; Mismatches 0; Indels
                                      Location/Qualifiers
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                                                                          /note= "alkylated"
                                                                                                                                                                                                                                     Disclosure; Page 3; 9pp; Japanese.
                                                       'note= "acylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "alkylated'
                                                                                                                                                                                                                                                                                                                                                                                                                              AAR29052 standard; peptide; 5 AA.
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                                                                                                                                                                   (FUJF ) FUJI PHOTO FILM CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (FUJF ) FUJI PHOTO FILM CO LTD.
                                                                                                                                  90JP-00333336,
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Best Local Similarity 100...
S; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide lipid contg.
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                                    Key
modified_site
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                                                               modified_site
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modified_site
                                                                                            JP04221395-A
                                                                                                                                29-NOV-1990;
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                  Synthetic
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Fibrinogen receptor antagonist; platelet aggregation; thrombosis; myocardial infarction.
                                                                                                                                  Fibrinogen receptor antagonising peptide (II).
                                                            AAR10414 standard; protein; 5 AA.
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                                                                                                                                                                                                                                                                                                                                                                                   Nutt RF, Brady SF,
CRGDC 5
                                                                                                                                                                                                                                  Disulfide-bond
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                                                                                                             10-APR-1991
                                                                                                                                                                                                                                                                                    30-JAN-1991
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                                                                                                                                                                                                Synthetic.
                                                                                    AAR10414;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        To residue N-MethylCys1 is attached Acetyl and to residue Cys5 is attached OH. The peptide is prepd. using standard methods of solid phase synthesis and is one of 17 pref. examples of a highly generic formula. The peptide is used to inhibit fibrinogen-induced platelet aggregation and is partic. useful because it does not significantly deplete the platelet count. It has a relatively short duration of activity and is thus useful where prevention of platelet aggregation over a short period of time is desirable, e.g. in surgery of peripheral arteries and cardiovascular surgery. It is also useful in prevention of platelet thrombosis, thromboembolism and reocclusion either during and after thrombolytic therapy, or after angioplasty of coronary and other arteries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and after coronary artery by-pass procedures, or to prevent myocardial infarction. It may be combined with thrombolytic agents, e.g. plasminogen activators or streptokinase, or anticoagulants. See also AAR10413-18 and EP-410537, EP-410539, EP-410540, EP-410541, and EP-410767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New fibrinogen receptor antagonising peptide cpds. - used to inhibit blood platelet aggregation during surgery on peripheral arteries and in cardiovascular surgery.
                         Gaps
                                                                                                                                                                                                                                    receptor antagonist; platelet aggregation; thrombosis;
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 Length 5;
                        0; Indels
100.0%; Score 35; DB 2; I
100.0%; Pred. No. 1.4e+06;
                                                                                                                                                                                                           Fibrinogen receptor antagonising peptide (III).
                         0; Mismatches
                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                    /label= N-MethylCys
                                                                                                                                    AAR10415 standard; protein; 5 AA.
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                         Conservative
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myocardial infarction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nutt RF, Brady SF,
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Query Match
Best Local Similarity
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Disulfide-bond
Modified-site
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                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                            AAR10415;
                         Matches
                                                                                                             RESULT 2
AAR10415
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Location/Qualifiers 1..5

(first entry)

90EP-00202015. 89US-00386534.

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To residue Cys5 is attached OH. The peptide is prepd. using standard methods of solid phase synthesis and is one of 17 pref. examples of a highly generic formula. The peptide is used to inhibit fibrinogen-induced platelet aggregation and is partic. useful because it does not significantly deplete the platelet count. It has a relatively short duration of activity and is thus useful where prevention of platelet enggragation over a short period of time is desirable. e.g. in surgery periodical arteries and cardiovascular surgery. It is also useful in prevention of platelet thrombosis; thromboembolism and reocclusion either during and after thrombolytic therapy, or after angioplasty of coronary and other arteries and after coronary artery by-pass procedures, or to prevent myocardial infarction. It may be combined with thrombolytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     agents, e.g. plasminogen activators or streptokinase, or anticoagulants. See also AAR10413-18 and EP-410539, EP-410540, EP-410541, and EP-410767
                                                                                                                                    New fibrinogen receptor antagonising peptide cpds. - used to inhibit blood platelet aggregation during surgery on peripheral arteries and in cardiovascular surgery.
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                                                                                                                                                                                                                                                                                 Claim 4; Page 10; 10pp; English.
Veber DF;
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                                                                      WPI; 1991-030928/05
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Best Local Similarity
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AAR10418
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AC AAR1
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Gaps

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6; Search time 121 Seconds (without alignments) 11.676 Million cell updates/sec
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Compugen Ltd.
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35
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Perfect score:
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries A\_Geneseq\_29Jan04:\*
1: geneseqp1980s:\*
2: geneseqp1990s:\*
3: geneseqp2000s:\* •• Database

geneseqp2003as:\* geneseqp2003bs:\* geneseqp2001s:\* geneseqp2002s:\* geneseqp2004s:\* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	Aar11587 Fibrinoge	Aar10415 Fibrinoge	Aar10414 Fibrinoge	Aar10418 Fibrinoge	Aar27031 Peptide 1		Aar69325 Gp_IIb/II	Aar79093 Alpha5/be	Aaw03492 Alpha(5)-	Aaw48499 Integrin	Aaw64952 Targettin	Aaw50594 GPIIb/III	Aay21570 Integrin-	_	Aay54976 Peptide l	_	Aae17982 Human lig	Abus9650 Finbronec	Aar76191 Alphav/be	Aaw03508 Alpha(5)-	Aaw03483 Alpha(5)-	Aaw35454 Non-dendr	Aaw35453 Non-dendr	Aay21561 Integrin-	Aay21586 Integrin-
QI	AAR11587	AAR10415	AAR10414	AAR10418	AAR27031	AAR29052	AAR69325	AAR79093	AAW03492	AAW48499	AAW64952	AAW50594	AAY21570	ADE25491	AAY54976	AAY95465	AAE17982	ABU59650	AAR76191	AAW03508	AAW03483	AAW35454	AAW35453	AAY21561	AAY21586
ength DB	5 2											2												9	
% Query Match Length	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
Score	35	35	35	35	35	35	35	35	35	35	35	35	35	35	35	35	35	35	35	35	35	35	35	35	35
Result No.		7	3	4	S	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25

Cys at position 1 carrries an acetyl group. The peptide inhibits binding of fibrinogen to the platelet membrane glycoprotein complex IIb/IIIa receptor. It may be used to prevent post-operative thromboesis, thromboembolism and reocclusion, platelet adhesion in extracorporeal blood circulation systems and to prevent myocardial infarction. See also AARI1584-6 and AARI1588-RI1594

Sequence 5 AA;

Aam48797 Tumour-ta Abu59535 Finbronec Abu59538 Finbronec Aay43232 RGD-conta			Aaw56034 Chimeric Aaw56035 Chimeric Aay5255 Synthetic Aay4233 RGD-CONTA	
	7 3 AAY90212 7 3 AAY90219 8 6 ABP98675 9 2 AAR79074 9 2 AAR76200	00000		1010
35 100.0 35 100.0 35 100.0	35 100.0 35 100.0 35 100.0		35 100.0 35 100.0 35 100.0	
222 287 387	10000000000000000000000000000000000000	3 9 7 8 6 2 8 7 8 6	2. 4. 4. 4. 2. 0 Ll 0 L	4 4 5 4 6

## ALIGNMENTS

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to prevent thrombosis,
                                                                         fibrinogen receptor antagonist; thrombosis; fibrinogen;
                                                                                                                                                                                                                                                          - used
                                                                                                                                                                                                                                                         Polypeptide fibrinogen receptor antagonists e.g. during cardiovascular surgery.
                                                                                                                                                                                                                             Duggan MF
                                                                                                            Location/Qualifiers 1. .5
                                                                                                                                    /label= Arg(phenyl)
                                                           Fibrinogen receptor antagonist #4.
                                                                                                                                                                                                                                                                                Disclosure; Page 7; 16pp; English.
              AAR11587 standard; protein; 5 AA.
                                                                                                                                                                                                                             Veber KF,
                                                                                                                                                                                 90EP-00311151.
                                                                                                                                                                                               89US-00421224.
                                            (first entry)
                                                                                                                                                                                                            (MERI ) MERCK & CO INC.
                                                                                                                                                                                                                             Nutt RF, Brady ST,
                                                                                                                                                                                                                                           WPI; 1991-111423/16.
                                                                                 IIb/IIIa receptor.
                                                                                                                    Disulfide-bond
Modified-site
                                                                                                                                                                                11-OCT-1990;
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                                            12-JUN-1991
                                                                                                                                                                  17-APR-1991.
                                                                                                                                                   EP422938-A.
                                                                                               Synthetic.
                             AAR11587;
RESULT 1
       AAR11587
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0; Gaps

Query Match 100.0%; Score 35; DB 16; Length 477; Best Local Similarity 100.0%; Pred. No. 41; Matches 5; Conservative 0; Mismatches 0; Indels 0

Search completed: September 22, 2004, 06:54:58 Job time : 117 secs

1 CRGDC 5 ||||| 444 CRGDC 448

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Query Match
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Matches 5; Conservative
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PEQUENCE FROM N.A.

PEQUENCE FROM N.A.

PEDLINE=22495039; PubMed=12606174;

MEDLINE=22495039; PubMed=12606174;

MEDLINE=22495039; PubMed=12606174;

Bentley S.D., Maiwald M., Murphy L.D., Pallen M.J., Yeats C.A.,

Bentley S.D., Maiwald M., Murphy L.D., Pallen M.J., Harris D.E.,

Nordercark H.G., Parkhill J., Relman D.A.,

Barrell B.G., Parkhill J., Lencet 361:637-644(2003).

Lancet 361:637-644(2003).

Lancet 361:637-644(2003).

BMBL, BASSI F. RATP binding; IEA.

GO; GO:0045255; C:hydrogen-translocating F-type ArPase complex; IEA.

GO; GO:0045254; F:ATP binding and phosphorylation-dependent c...; IEA.

RO; GO:0045254; F:ATP-binding and phosphorylation-dependent c...; IEA.

RO; GO:004533; F:hydrogen-exporting ATP synthase activity, phospho...; IEA.

RO; GO:0046933; F:hydrogen-transporting ATP synthase activity...; IEA.
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Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.

BMBL; AF483648; AA084483.1; -...

BMBL; AF483648; AA084483.1; -...

BMBL; AF483648; AA084483.1; -...

BMBC; GO:0005524; F:ATP binding; IEA.

GO; GO:0005224; F:ATP binding and phosphorylation-dependent c. .; IEA.

RO; GO:0005224; F:ATP-binding and phosphorylation-dependent c. .; IEA.

RO; GO:0005224; F:ATP-binding and phosphorylation-dependent c. .; IEA.

RO; GO:000166; F:ATP-binding and phosphorylation-dependent c. .; IEA.

RO; GO:000166; F:ATP-synthesis coupled ATP synthase activity. .; IEA.

RO; GO:0015929; F:Proton transport; IEA.

RO; GO:0015929; P:Proton transport; IEA.

RO; GO:0015929; P:Proton transport; IEA.

RO; GO:0015929; AAA ATPase.

RITERPO; IPR001014; ATPase. a/bc.

RITERPO; IPR001014; ATPase. a/bc.

RITERPO; IPR001013; ATPase. a/bc.

RITERPO; IPR001003; ATPase. a/bc.

RITERPO; IPR001005; RI ATPase. a/bN.

REAM; PP00306; ATP-synt_ab; I.

REAM; PP00306; ATP-synt_ab.; I.

REAM; PP00306; ATP-synt_ab.N; I.

REAM; PP00306; ATP-synt_ab.N; I.
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                                                                                                                                                                                                                                      Maiwald M., Lepp P.W., Relman D.A.;
"Analysis of conserved non-rRNA genes of Tropheryma whipplei:
implications for genome structure, strain typing, and phylogenetic
                 Tropheryma whipplei (Whipple's bacillus) (Tropheryma whippelii).
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Micrococcineae; Cellulomonadaceae; Tropheryma.
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Bacteria, Actinobacteria; Actinobacteridae; Actinomycetales; Micrococcineae; Cellulomonadaceae; Tropheryma.
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 25, Last annotation update)
ATP synthase beta chain (EC 3.6.3.14).
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Best Local Similarity 100...
S; Conservative
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01-JUN-2003
01-JUN-2003
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DR GO, GO. 1001936; F. Phydrolase activity; IEA.

DR GO, GO. 1001976; F. Phydrolase activity; IEA.

DR INGERFO; PRO00131; APPERS A. Phydrolase; C. Phydrolase; Phydrolas
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Gaps

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Length 336;

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Makana T., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Azawa T., Itawa M., Nishi K., Kiyosawa H., Konko S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Reischmann W., Gasterland T., Gissi C., King B., Kochiwa H., Schrim L.M., Esaubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Bronstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N. H., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamcto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Winnhaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Narahisaki V., Vanani V., Wanning L., Wanniani V., Wanniani V., Kawahi H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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"Functional annotation of a full-length mouse cDNA collection.";
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   Hypothetical protein.
SEQUENCE 336 AA; 37667 MW; FD51D95493576F71 CRC64;
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Ol-MAR-2003 (TrEMBLrel. 13, Last sequence update)
1500016010Rik protein (Fragment).
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
ATP synthase Fl complex beta chain.
                                                                                           100.0%; Score 35; DB 4;
100.0%; Pred. No. 30;
iive 0; Mismatches 0,
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STRAIN=C57BL/6J; TISSUE=Cerebellum;
MEDLINE=21085660; PubMed=11217851;
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MGD; MGI:1916202; 1500016010Rik.
InterPro; IPR006634; TLC.
                                                                                                  Query Match 100.
Best Local Similarity 100.
Matches 5; Conservative
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Q84DX6;
01-JUN-2003 (
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Q84DX6
ID Q84DX
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DE ATP 8
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MEDLINE=21465035; PubMed=11581380;

MEDLINE=21465035; PubMed=11581380;

A Powerte A.M., Brault A.C., Shirako Y., Strauss E.G., Kang W.,

Strauss J.H., Weaver S.C.;

I "Evolutionary relationships and systematics of the alphaviruses.";

I J. Virol. 75:10118-10131(2001).

I MALISTRAIN A. MEANOR S.G. STRUCTURAL MOLECULE activity; IEA.

R GO; GO:0005198; F:structural molecule activity; IEA.

R InterPro; IPR000536; Alpha_El_glycop.

R InterPro; IPR000336; FlatiglycoprotE.

R InterPro; IPR00110; Ig-like.

R Pfam; PF01589; Alpha_El_glycop; 1.
                                                                                                     Gaps
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Viruses: ssRNA positive-strand viruses, no DNA stage; Togaviridae;
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QBNCQ7.
01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Hypothetical protein.
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                 100.0%; Score 35; DB 12; Length 279; 100.0%; Pred. No. 26; ive 0; Mismatches 0; Indels (
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Strausberg R.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC029574; AAH29574.1; -
GO; GO:0005509; F:calcium ion binding; IEA.
GO; GO:0016042; F:chospholipase A2 activity; IEA.
GO; GO:0016042; P:lipid catabolism; IEA.
InterPro; IPR001211; PhospholipaseA2.
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36014 MW; A584EAC07D3948AE CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
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Query Match
Best Local Similarity 100.v.
S; Conservative
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nes 5; Conservative
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335 AA;
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SEQUENCE FROM N.A.
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NON TER
SEQUENCE
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Matches
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SEQUENCE FROM N.A. MEDIANG=12139629; MEDLINE=22136043; PubMed=12139629; Rlein R., Baranyi U., Rossler N., Greineder B., Scholz H., Witte A.; Ricin R., Baranyi U., Rossler N., Greineder B., Scholz H., Witte A.; Matrialba magadii virus phiChi: first complete nucleotide sequence and functional organization of a virus infecting a haloalkaliphilic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=20177831; PubMed=10712697;

Baranyi U., Klein R., Lubitz W., Kruger D.H., Witte A.;

"The archaeal halophilic virus-encoded Dam-like methyltransferase M.
phiChl-I methylates adenine residues and complements dam mutants in
the low salt environment of Escherichia coli.";

Mol. Microbiol. 35:1168-1179(2000).
[1]
SEQUENCE FROM N.A.
Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Jones K.M., Overton II L.L., Tsitrin T., Kim M.M., Bera J.J., Jin S.S., Fadrosh D.W., Tallon L.J., Koo H., Zismann V., Haisiao J., Blunt S., Vanaken S.S., Riedmuller S.B., Utterback T.T. Feldblyum T.V., Yang O.O., Haas B.J., Suh B.B., Peterson J.J., Quackenbush J., White O., Salzberg S.L., Fraser C.M., "Oryza sativa chromosome 3 BAC OSJNBa0042109 genomic sequence."; Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae.
NCBL_TaxID=114777;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 35; DB 10; Length 218; 100.0%; Pred. No. 21;
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MEDLINE=20497008; PubMed=11040128;
Klein R., Greineder B., Baranyi U., Witte A.;
"The structural protein E of the archaeal virus phiChl: evprocessing in Narrialba magadii during virus maturation.";
Virology 276:376-387(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
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PROSITE; PS50157; ZINC_FINGER_C2H2_2; 2.
Hypothetical protein; Metal-binding; Zinc; Zinc-finger.
SEQUENCE 279 AA; 31698 MW; 2A47BFE882306E13 CRC64;
                                                                                                                                                                                                                                                                                                                                                       Emba, According Hypothetical protein. SEOUENCE 218 AA; 24562 MW; 4FEOA501A4A17507 CRC64;
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24, Last annotation update)
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IX MEDLINE=22154683; PubMed=12466851;

A The FANTOM Consortium,

A the FANTOM Consortium,

A the RIKEN Genome Exploration Research Group Phase I & II Team;

A the RIKEN Genome Exploration Research Group Phase I & II Team;

To 770 full-length cDNAs.";

IN Nature 420:563-5712002).

R GO, 700 full-length cDNAs.";

NR EMBL; AK004035; BAC25063.1; -

R GO, GO:0008415; Facyltransferase activity; IEA.

R GO, GO:0008415; Facyltransferase.

R GO, GO:0008415; Facyltransferase.

InterPro; IRR002123; Acyltransferase.

R InterPro; IRR00979; Tafazzin.

R InterPro; IRR00979; Tafazzin.

R FAMT; SM00563; PlSC; 1.

SR SMART; SM00563; PlSC; 1.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopaida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
NCBI_TaxID=39947;
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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         Moravec T., Cerovska N., Pecenkova T., Nielsen S.L., Vlcek C.;
                                                                                                                                                                                                                                          100.0%; Score 35; DB 12; Length 119; 100.0%; Pred. No. 12;
                               "The nucleotide sequence of potato mop-top isolate 54-15."; Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY187010; AA032789.1; ...
InterPro; IPR0011996; Plant vir prot.
Pfam; PF01307; Plant vir prot; ISEQUENCE 119 AA; I3154 MW; D2D37E6768305932 CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
11-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein.
OSJNBA0042109.11.
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Best Local Similarity 100..
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MEDIINE=95088602; PubMed=7996148;
Scott K.P., Kashiwazaki S., Reavy B., Harrison B.D.;
The nucleotide sequence and poteto mop-top virus RNA 2: a novel type of genome organization for a furovirus.";
J. Gen. Virol. 75:3561-3568[1994].
EMBL; D30753; BAA06413.1; -.
InterPro; IPR001896; Plant vir prot.
Prom; PF01307; Plant vir prot.
Probom; P0001561; Plant vir prot; 1.
Probom; P0001561; Plant vir prot; 1.
SEQUENCE 119 AA; 13109 MW; CF136F869821B8C2 CRC64;
                                                                                                                             STRAIN=Swedish:
Savedish:
Savenkov E.I., Sandgren M., Germundsson A.;
Savenkov E.I., Sandgren M., Germundsson A.;
Submitted Sequence of RNA2 from Potato mop-top virus (PMTV-Sw).";
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ277556; CAB91102.1; -.
InterPro; IPR001896; Plant vir prot.
Probom; PD001561; Plant vir prot; 1.
Probom; PD001561; Plant vir prot; 1.
SEQUENCE 119 AA; 13123 MW; CF15C8BC03305932 CRC64;
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Viruses; ssRNA positive-strand viruses, no DNA stage; Pomovirus.
VCBI_TaxID=37128;
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Viruses; BSRNA positive-strand viruses, no DNA stage; Pomovirus.
VCBI_TaxID=37128;
                      ssRNA positive-strand viruses, no DNA stage; Pomovirus
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01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Triple gene block protein 13K.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Potato mop-top virus
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                                                NCBI_TaxID=37128;
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NCBI_TaxID=71972;
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Viruses; ssRNA positive-strand viruses, no DNA stage; Pomovirus
NCBI_TaxID=79918;
                                                                                                                                                                                                                                                                                         MEDLINE=98378056; PubMed=9714254;
MEDLINE=98378056; PubMed=9714254;
Meoning R., Plaid C., Beier C., Commandeur U.;
"Genome properties of beet virus Q, a new furo-like virus from sugarbeet, determined from unpurified virus.";
J. Gen. Virol. 79:207-2036 (1998).
EMBL, AJ223598; CAA11463.1;
InterPro; IPR001896; Plant_vir_prot.
Pfam; PP01307; Plant_vir_prot.]
Probom; P000156; Plant vir prot; 1.
SEQUENCE 118 AA; 12779 MW; A55EF6BC198123EB CRC64;
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Q91V53,
Q1-OCT-2000 (TrEMBLrel. 15, Created)
O1-OCT-2000 (TrEMBLrel. 15, Last sequence update)
O1-UNM-2003 (TrEMBLrel. 24, Last annotation update)
Triple-gene-block protein 2.
                                                                                                         01-NOV-1998 (TrEMBLrel. 08, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update) Second triple gene block gene.
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Triple-gene-block second protein.
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01-NOV-1998 (TrEMBLrel. 08,
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Q9YPH2; Q9YPH2

ò 유 RESULT 3
Q9YPH2
ID Q9YPH2
DT Q9YPH
DT 01-M
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Gaps

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Query Match

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ઠે 셤 RESULT 4
091V53
ID 091V;
AC 091V,
DT 01-0
DT 01-0
DT 01-0
DT Trip

SEQUENCE FROM N.A. STRAIN=54-15;

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RESULT
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O3751 Decod bean
O31953 potato mop-
08692 potato mop-
086m2 mus musculu
085m3 orga sativ
08135 virus phich
08v35 ag80-663 vi
08v35 ag80-663 vi
09cw26 mus musculu
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09cw26 mus ropheryma
08391 tropheryma
08391 tropheryma
08391 tropheryma
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O92517 beet virus
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                                                          September 22, 2004, 06:47:32; Search time 115 Seconds (without alignments) 13.718 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Description
GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                               1017041 seqs, 315518202 residues
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                                         OM protein - protein search, using sw model
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092517
091V53
Q81V53
Q85292
Q80QA2
Q851N3
Q851N3
Q81J35
Q8VA50
Q8NCQ7
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Q83HY0
Q83G91
Q80IB8
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1: Sp archea:*
2: Sp_bacteria:*
3: Sp fungi:*
4: Sp_human:*
5: Sp_invertebrate:*
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8p_organelle:*
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Gapop 10.0 , Gapext 0.5
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Maximum Match 100%
Listing first 45 su
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sp_bacteriap:*
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Q80ia8 influenza a Q80ic9 influenza a Q80ic9 influenza a Q80ib9 influenza a Q80ib9 influenza a Q80ib1 influenza a Q80ib1 influenza a Q80ib1 influenza a Q80ib1 influenza a Q80ib2 influenza a Q80ib2 influenza a Q96747 influenza a Q96747 influenza a Q96749 influenza a Q9675 venezuelan Q99xc5 venezuelan Q98815 eastern equ Q88816 eastern equ Q88816 eastern equ Q88817 eastern equ Q88819 eastern equ Q88818 eastern equ Q88821 eastern equ Q88822 eastern equ Q88822 eastern equ
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Q80197
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Q9GYG8
Q9WC27
Q8AYF9
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Q88808
Q88818
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Q88807
Q88804
Q88822
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## ALIGNMENTS

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STRAIN=10365;
MEDLINE=94076404; PubMed=8254725;
Weaver S.C., Hagenbaugh A., Bellew L.A., Gousset L., Mallampalli V.,
Holland J.J., Scott T.W.;
"Evolution of alphaviruses in the eastern equine encephalomyelitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                 08801;
01-NOV-1996 (TrEWBLrel. 01, Created)
01-NOV-1996 (TrEWBLrel. 01, Last sequence update)
01-OCT-2003 (TrEWBLrel. 25, Last annotation update)
El protein (Fragment).
Eastern equine encephalitis virus (Eastern equine encephalomyelitis
                                                                                                                                                                                    Viruses; ssRNA positive-strand viruses, no DNA stage; Togaviridae;
Alphavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88 AA; 9540 MW; CBB34D04C62C196F CRC64;
88
                                                                                                                                                                                                                                                                                                                                                                                                                          complex.";
J. Virol. 68:158-169(1994).
EMBL; U01577; AAC53764.1; -
INTERPRO; IPR002548; Alpha El_glycop.
InterPro; IPR007110; Ig-like.
Pfam; PP01589; Alpha El_glycop.
PRT;
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PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
Les 5; Conserv
                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                 NCBI_TaxID=11021;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=93187617; PubMed=8445371; Sneider J.M., Kinney R.M., Tsuchiya K.R., Trent D.W.; Sneider J.M., Kinney R.M., Tsuchiya K.R., Trent D.W.; Sneider J.M., Kinney R.M., Tsuchiya K.R., Trent D.W.; Molecular evidence that epizootic Venezuelan equine encephalitis "Molecular evidence that epizootic Venezuelan equine encophalitis subtype I-B or II viruses."; J. Gen. Virol. 74:519-523 (1993).

-I. FUNCTION: THE CARSID PROTEIN IS AN AUTO-PROTEASE.

-I. PTM: Specific enzymatic cleavages in vivo yield mature proteins.

-I. PTM: SECELLAMBOUS: THE G kDa POLYPEPTIDE PROBABLY SERVES AS THE SIGNAL SEQUENCE FOR THE MEMBRANE GLYCOPROTEIN E1, WHICH IS THE VIRAL HEMAGGLUTININ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-1994 (Rel. 29, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Structural polyprotein (P130) (Contains: Coat protein C (EC 3.4.21.-)
(Capsid protein C); Spike glycoprotein E3; Spike glycoprotein E2;
Venezuelan equine encephalitis virus (strain Mena II).
Viruses; ssRNA positive-strand viruses, no DNA stage; Togaviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
6 kDa PEPTIDE.

SPIKE GLYCOPROTEIN E1.

CHARGE RELAY SYSTEM (BY SIMILARITY).

POTENTIAL.

POTENTIAL.

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 32; DB 1; Length 125
Pred. No. 1.1e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                             MW; 29DDEF37F9E92C4B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POLS EEVVM STANDARD; PRT; 1254 AA. P36331; Q66587; Q66589; Q66590; Q66591; Q01-UUN-1994 (Rell. 29, Created) 01-UUN-1994 (Rell. 29) Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro, IPR002548; Alpha E1 glycop.
InterPro, IPR000336; Alpha E2 glycop.
InterPro; IPR002533; Alpha E3 glycop.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; L04599; AAA42990.1; -.
EMBL; L04599; AAA42991.1; ALT_ERM
EMBL; L04599; AAA42991.1; ALT_SEQ.
EMBL; L04599; AAA42992.1; ALT_SEQ.
EMBL; L04599; AAA42993.1; ALT_SEQ.
EMBL; L04599; AAA42994.1; ALT_SEQ.
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HSSP; P03315; 1VCP.
MEROPS; S03.001; -.
                                                                                                                                                                                                                                                                                                                                                                                             1254 AA;
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                                                                                                    Transmembrane; Glycoprotein; Hydrolase;
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SIMILARITY).
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(POTENTIAL).
(POTENTIAL).
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Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                138343 MW; FB9DE88265F20211 CRC64;
                                                                                                                                                                                   CHARGE RELAY SYSTEM (BY
CHARGE RELAY SYSTEM (BY
CHARGE RELAY SYSTEM (BY
                                                                                                                          COAT PROTEIN C.
SPIKE GLYCOPROTEIN E3.
SPIKE GLYCOPROTEIN E2.
6 kDa PEPTIDE.
SPIKE GLYCOPROTEIN E1.
                                                                                                                                                                                                                                                       N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
                                                                                                                                                                                                                                                                                         (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                           completed: September 22, 2004, 06:52:12
                                                                                                                                                                                                                                                                                         N-LINKED (
InterPro; IPR009003; Cye Ser trypsin.
InterPro; IPR000336; Flavi glycoprotE.
InterPro; IPR007110; Ig-like.
                                                                                                                                                                                                                     POTENTIAL
                                                                                                                                                                                                                                 POTENTIAL
          InterPro; IPR000336; Flavi glycoprot InterPro; IPR000136; Flavi glycoprot InterPro; IPR0001010; Ig-like.

InterPro; IPR000910; Peptidase_S3.

Pfam; PF00184; Alpha_Core; 1.

Pfam; PF00189; Alpha_E_J-yrcop; 1.

Pfam; PF01563; Alpha_E3_glycop; 1.

Pfam; PF01563; Alpha_E3_glycop; 1.

PRINTS; PR007798; TOGAVIRIN.

Cat protein; Polyprotein; Transmemb Serine protease.
                                                                                                                                                                                                                                                                                                                                      91.4%;
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Best Local Similarity
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POLS EEVVE
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                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                  J. Gen. Virol. 67:1951-1960(1986).
-!- FUNCTION: THE CAPSID PROTEIN IS AN AUTO-PROTEASE.
-!- PTM. Specific enzymatic cleavages in Vivo yield mature proteins.
-!- RISCELLANEOUS: THE 6 kDa POLYPEPTIDE PROBABLY SERVES AS THE SIGNAL
SEQUENCE FOR THE MEMBRANE GLYCOPROTEIN B1, WHICH IS THE VIRAL
HEMAGGLUTININ.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Interpro; PRO00548; Alpha El glycop.

DR Interpro; IPR000534; Alpha E2_glycop.

R Interpro; IPR000533; Alpha E2_glycop.

R Interpro; IPR000903; Cys Ser trypsin.

R Interpro; IPR000903; Cys Ser trypsin.

R Interpro; IPR00091; Ig-like.

R Interpro; IPR00091; Ig-like.

R Interpro; IPR000930; Peptidase_S3.

R Interpro; IPR000930; Peptidase_S3.

R Ffam; PF00943; Alpha E1_glycop; 1.

R Ffam; PF01543; Alpha E2_glycop; 1.

R Pfam; PF01543; Alpha E2_glycop; 1.

R Pfam; PF01543; Alpha E2_glycop; 1.

R Pfam; PR01543; Alpha E2_glycop; 1.

R RINTS; PR00798; TOGAVIRIN.

W Coat protein; Polyprotein; Transmembrane; Glycoprotein; Hydrolase; M Serine protease.
                                        SEQUENCE FROM N.A. MEDLINE=86306669; PubMed=3755750; Johnson B.J.B., Kinney R.M., Koet C.L., Trent D.W.; Molecular determinants of alphavirus neurovirulence: nucleotide and deduced protein sequence changes during attenuation of Venezuelan equine encephalitis virus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPIKE GLYCOPROTEIN E3.
SPIKE GLYCOPROTEIN E2.
6 kDa PEPTIDE.
SPPIKE GLYCOPROTEIN E1.
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
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N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                    SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY S3.
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                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        652 65
946 94
1254 AA;
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MEROPS; S03.001;
                                                                                                                                  Alphavirus.
NCBI_TaxID=11037;
                      EEW8
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RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Subtype 1-E or II viruses.";
J. Gen. Virol. 74:519-522(1993).
-!- FUNCTION: THE CARSID PROTEIN IS AN AUTO-PROTEASE.
-!- PTM: Specific enzymatic cleavages in vivo yield mature proteins.
-!- MISCELLANEOUS: THE 6 KDB POLYPEPTIDE PROBABLY SERVES AS THE SIGNAL SEQUENCE FOR THE MEMBRANE GLYCOPROTEIN E1, WHICH IS THE VIRAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein C (EC 3.4.21.-)
                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=93187617; PubMed=8445371; Sneider J.W.; Kinney R.M., Tacht D.W.; Kinney R.M., Tacht B.W.; Hauchiya K.R., Trent D.W.; Woldecular evidence that epizootic Venezuelan equine encephalitis (VEE) I.AB viruses are not evolutionary derivatives of enzootic VEE
                                                                                                                                                                                                                                                                                                                                                                                                      POLS EEVVE STANDARD; PRT; 1254 AA.
P36330; Q66582; Q66583; Q66586; Q66586;
P36330; Q66582; Q66583; Q66584; Q66586;
O1-UTN-1994 (Rel. 29, Last sequence update)
O1-UTN-1994 (Rel. 29, Last amotation update)
Structural polyprotein (P130) [Contains: Coat protein C (EC 3.4.21)
Gapsid protein C); Spike glycoprotein E3; Spike glycoprotein E2;
6 kDa peptide; Spike glycoprotein E1].
Venezuelan equine encephalitis virus (strain Everglades Fe3-7C).
Viruses; SSRNA positive-strand viruses, no DNA stage; Togavizidae;
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Serine protease.
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   Length 1254;
                                                                         0; Indels
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SPIKE GLYCOPROTEIN E3.
SPIKE GLYCOPROTEIN E2.
91.4%; Score 32; DB 1; 180.0%; Pred. No. 1.1e+02;
                                                                         1; Mismatches
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EMBL; L04598; AAA42983.1; ALT TERM.
EMBL; L04598; AAA42985.1; ALT SEQ.
EMBL; L04598; AAA42986.1; ALT SEQ.
EMBL; L04598; AAA42988.1; ALT SEQ.
EMBL; L04598; AAA42988.1; ALT SEQ.
EMBL; L04598; AAA42988.1; ALT INIT.
FIR; J01978; J01978.
HSSP; P03315; 1VCP.
                                      Best Local Similarity 80.0
Matches 4; Conservative
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1188 CKGDC 1192
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SEQUENCE
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                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lab-sib.ch).
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"Nucleotide sequence of the genome region encoding the 26S mRNA of eastern equine encephalomyelitis virus and the deduced amino acid sequence of the viral structural proteins.";

J. Gen. Virol. 68:2129-2142[1987).

-!- FUNCTION: THE CAPSID PROTEIN IS AN AUTO-PROTEASE.

-!- PINTS Specific enzymatic cleavages in vivo yield mature proteins.

-!- MISCELLANEOUS: THE 6 kDs POLYPEPTIDE PROBABLY SERVES AS THE SIGNAL.

SEQUENCE FOR THE MEMBRANE GLYCOPROTEIN B1, WHICH IS THE VIRAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
16-AUG-1992 (Rel. 24, Last annotation update)
16-CCT--2001 (Rel. 40, Last annotation update)
Structural polyprotein (Pl30) [Concains: Coat protein C (EC 3.4.21.-)
(Capsid protein C); Spike glycoprotein E3;
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SPIKE GLYCOPROTEIN E3.
SPIKE GLYCOPROTEIN E2.
6 KDA PEFTIDE.
SPIKE GLYCOPROTEIN E1.
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                Coat protein; Polyprotein; Transmembrane; Glycoprotein; Hydrolase;
Serine protease.
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N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
MW; 8C7664A405D2D41C CRC64;
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                                                                                                          SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY S3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 32; DB 1; Length 1239;
Pred. No. 1.1e+02;
1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                      InterPro; 1978002948; Alpha El glycop. InterPro; IPR0002948; Alpha E2 glycop. InterPro; IPR000936; Alpha E2 glycop. InterPro; IPR0009003; Cys Ser trypsin. InterPro; IPR0009103; Cys Ser trypsin. InterPro; IPR0009110; Ig-like. InterPro; IPR000930; Peptidase_S3. Pfam; PF00944; Alpha core; 1. Pfam; PF00943; Alpha E1 glycop; 1. Pfam; PF01569; Alpha E1 glycop; 1. Pfam; PF01563; Alpha E2 glycop; 1. Pfam; PF01563; Alpha E3 glycop; 1. Pfam; PF01563; Alpha E3 glycop; 1. Pfam; PF01563; Alpha E3 glycop; 1.
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80.0%;
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1239 AA; 137431
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                                                                                              HEMAGGLUTININ
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation — the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  North America.";
Virology 182:774-784 (1991).
Virology 182:774-784 (1991).
--- FUNCTION: THE CAPSID PROTEIN IS AN AUTO-PROTEASE.
--- PTM: Specific enzymatic cleavages in vivo yield mature proteins.
--- PTM: Specific enzymatic cleavages in vivo yield mature proteins.
--- MISCELLANEOUS: THE 6 KDa POLYPEPTIDE PROBABLY SERVES AS THE SIGNAL SEQUENCE FOR THE MEMBRANE GLYCOPROTEIN E1, WHICH IS THE VIRAL
6 kDa peptide; Spike glycoprotein El].
Bastern equine encephaltis virus (strain val3[ten broeck]) (Eastern
equine encephalomyellits virus).
Viruses; ssRNA positive-strand viruses, no DNA stage; Togaviridae;
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                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=912207277: PubMed=2024496;
Weaver S.C., Scott T.W., Rico-Hesse R.;
"Molecular evolution of eastern equine encephalomyelitis virus in
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CHARGE RELAY SYSTEM (BY SIMILARITY)
FOTENTIAL.
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-!- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY S3.
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Pred. No. 1.1e+02;
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N-LINKED (GLCNAC. . .)
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SPIKE GLYCOPROTEIN E2.
6 KDA PEPTIDE.
SPIKE GLYCOPROTEIN E1.
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InterPro; IPR001548; Alpha_E2_glycop.
InterPro; IPR001548; Alpha_E2_glycop.
InterPro; IPR001548; Alpha_E2_glycop.
InterPro; IPR001548; Flavi, glycop.
InterPro; IPR001109; Ig-like.
InterPro; IPR001110; Ig-like.
InterPro; IPR001109; Ig-like.
INTERPRO; IRR001109; Ig-like.
INTERPRO; IRR001109; Ig-like.
IRR00110
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80.0%;
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933 93
1240 AA;
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Best Local Similarity
                                                                                                                                                                                             Alphavirus.
NCBI_TaxID=11022;
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01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Structural polyprotein (P130) [Contains: Coat protein C (EC 3.4.21.-)
(Capsid protein C); Spike glycoprotein B3; Spike glycoprotein E2;
6 kDa peptide; Spike glycoprotein B1.
Eastern equine encephalitis virus (Eastern equine encephalomyelitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Viruses; ssRNA positive-strand viruses, no DNA stage; Togaviridae;
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    SMART; SM00094; TR FER; 2.
PROSITE; PS00205; TRANSFERIN 1; 2.
PROSITE; PS00206; TRANSFERIN 2; 2.
PROSITE; PS00207; TRANSFERIN 3; 1.
Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
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1 (BY SIMILARITY).
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CARBONATE 2 (BY SIMILARITY).
CARBONATE 2 (VIA AMIDE NITROGEN)
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Pred. No. 64;
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STRAIN-82V-2137;
MEDLINE-87282265; PubMed=2886548;
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80.0%;
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Kvingedal A.M., Roervik K.A., Alestroem P.;
"Cloning and characterization of Atlantic salmon (Salmo salar) serum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Salmo salar (Atlantic salmon).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostei, Buteleostei,
Protacanthopterygii, Salmoniformes, Salmonidae, Salmo.
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-!- SUBURIT: Monomer.
-!- SUBURIT: Monomer.
-!- SUBURIT: Alocation Secreted.
-!- SUBURIT: Alocation in liver and serum with smaller amounts found in the stomach and kidney.
-!- DOMAIN: Composed of two homologous domains.
-!- SIMILARITY: Belongs to the transferrin family.
HSSP; P56410; IAOV.
IRON 1 (BY SIMILARITY).
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1 (VIA AMIDE NITROGEN)
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Pred. No. 64;
                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
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01-NOV-1995 (Rel. 32, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Serotransferrin II precursor (Siderophilin II) (STF II)
                                                                                                                                                                                                                                                                                                                                    2F996CA1AEE79570 CRC64;
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1; Mismatches
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Pfam; PF00405; transferrin; 2.
PRINTS; PR00422; TRANSFERRIN.
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Local Similarity 80.0%;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                degradation to
may also have
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R EMBL; L25909; AAC42221.1; -.

R PIR; 151350, 151350.

R HSSP; P56410; 1AOV.

R HSSP; P56410; 1AOV.

R InterPro; IPR001156; Transferrin. 2.

R PRINTS; PR00405; TRANSFERRIN.

R PRINTS; SN00094; TR FER; 2.

R PROSITE; PS00206; TRANSFERRIN 1; 2.

R PROSITE; PS00206; TRANSFERRIN 2; 2.

R PROSITE; PS00207; TRANSFERRIN 3; 1.

R PROSITE; PS00207; TRANSFERRIN 3; 1.

R Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
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                                                                                                                               SUBUNIT: Monomer.
SUBCELLULAR LOCATION: Secreted.
TISSUE SPECIFICITY: Abundant in liver and serum with smaller amounts found in the stomach and kidney.
DOMAIN: Composed of two homologous domains.
SIMILARITY: Belongs to the transferrin family.
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of an anion, usually bicarbonate. It is responsible transport of iron from sites of absorption and heme those of storage and utilization. Serum transferrin a further role in stimulating cell proliferation.
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   SOLUTION TO THE STATE ST
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DB 1; Length 690;

Score 32;

91.48;

Query Match

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                                                                                                                                                                                                                                                                                                                                                 MEDALINE=96414927; PubMed=8817928; Mikawa N., Hirono I., Aoki T.; Mol. Mar. Biol Tendenhol. 5:225-229(1996).

-I. FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH CAN BIND TWO ATOMS OF PERRIC IRON IN ASSOCIATION WITH THE BINDING OF AN ANION, USUMLLY BICARBONATE.

-I. SUBUNIT: Monomer (By similarity).
-I. SUBCELMULAR LOCATION: Secreted.
-I. DOMAIN: Composed of two homologous domains.
-I. SIMILARITY: Belongs to the transferrin family.
                  Gaps
                                                                                                                                                                                                                      Serotransferrin precursor.
Oryzias latipes (Medaka fish) (Japanese ricefish).
Bukaryota, Metazoa; Chordata, Craniata, Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neotteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
Beloniformes; Adrianichthyidae; Oryzinae; Oryzias.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001156; Transferrin.
Pfam, PF00405; transferrin; 2.
PRINTS; PR004022; TRANSFERIN.
SWART; SM00094; TR FER; 2.
PROSITE; PS00205; TRANSFERIN 1; 2.
PROSITE; PS00206; TRANSFERIN 2; 2.
PROSITE; PS00207; TRANSFERIN 3; FALSE NGG.
Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
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(Rel. 38, Last sequence update)
(Rel. 42, Last annotation update)
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   Pred. No. 64;
1; Mismatches
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IRON 1
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                  Conservative
                                                                                                                                                STANDARD;
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Matches 4, Conserv
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186 CKGDC 190
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                                             1 CRGDC 5
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ID TRFE ORYLA
AC P79819;
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-!- SIMILARITY: Belongs to family 3 of glycosyl hydrolases.
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360 3
654 AA;
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P80426;
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SEQUENCE
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         and for commercial
                          (See http://www.isb-sib.ch/announce/
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-!- CATALYTIC ACTIVITY: Hydrolysis of 1,4-beta-D-xylans so as to remove successive D-xylose residues from the non-reducing termini.
-!- SUBCELLUIAR LOCATION: Periplasmic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=95198684, PubMed=7891660,
Vroemen S., Heldens J., Boyd C., Henrissat B., Keen N.T.;
"Cloning and characterization of the bgxA gene from Erwinia
chrysanthemi DI which encodes a beta-glucosidase/xylosidase enzyme.";
Mol. Gen. Genet. 246:465-477(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Beta-glucosidase (EC 3.2.1.21) (Gentiobiase) (Cellobiase); Beta-
xylosidase (EC 3.2.1.37) (1,4-beta-D-xylan xylohydrolase) (Xylan 1,4-
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10.NOV-1997 (Rel. 35, Created)

10.NOV-1997 (Rel. 35, Last sequence update)

28.FEB-2003 (Rel. 41, Last annotation update)

28.FEB-2003 (Rel. 41, Gest annotation update)

Periplasmic beta-glucosidase/beta-xylosidase precursor [Includes:
Periplasmic beta-glucosidase/beta-xylosidase); Beta-

Periplasmic beta-glucosidase(Rel 3.2.1.21) (Gentiobiase) (Cellobiase); Reyan 1
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Enterobacteriaceae; Pectobacterium.
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-!- FUNCTION: EXHIBITS BOTH BETA-GLUCOSIDASE AND BETA-XYLOSIDASE
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BY SIMILARITY.
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N.LINKED (GLCNAC...) (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 454;
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modified and this statement is not removed. Usage entities requires a license agreement (See http://wwor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                         SMART; SM0204; TGFB; 1.
PROSITE; PS00250; TGF BETA 1; 1.
Growth factor; Cytokine; Glycoprotein; Signal.
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Pred. No. 44;
1; Mismatches
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                                                                                              EMBL; AC004500; AAC08450.1; -. HSSP; P12643; 3BMP. Genew; HGNC:4224; GDF9.
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80.0%;
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PRINTS; PR00669; INHIBINA.
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382 CKGDC 386
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"Immunoassay and partial characterization of serum transferrin from
Atlantic salon (Salmo salr L.).";
Fish Shellish Immunol. 5:71-80(1995).
-!- FUNCTION: Transferrins are iron binding transport proteins which
can bind two atoms of ferric iron in association with the binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kvingedal A.M., Roervik K.A., Alestroem P.; "Cloning and characterization of Atlantic salmon (Salmo salar) serum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Salmo salar (Atlantic salmon).
Salmo salar (Atlantic salmon).
Medizogoa, Chordata, Craniata, Vertebrata, Euteleostomi, Actinopterygii, Neopterygii, Teleostei, Euteleostei, Protacanthopterygii, Salmoniformes, Salmonidae, Salmo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Characterization of the 5' region of the Atlantic salmon (Salmo salar) transferrin-encoding gene.";
Gene 150:335-339(1994).
                                                                                                                                                                 POTENTIAL.
PERIPLASMIC BETA-GLUCOSIDASE/BETA-
XYLOSIDASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 654;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                        BY SIMILARITY.
BY SIMILARITY.
5CEDFE62162A7A95 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Serotransferrin I precursor (Siderophilin I) (STF I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 32; DB 1
Pred. No. 61;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         690 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mol. Mar. Biol. Biotechnol. 2:233-238(1993)
                                                                                                                                      EMBL; U08606; AAA80156.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Liver;
MEDLINE=94122797; PubMed=8293074;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1-64 FROM N.A.
MEDLINE-95121925; PubMed=7821802;
                                                                                                                                                                                                                                                                                                                                                                                                               71584 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                               91.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity 80.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
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OTHER MEMBERS OF THIS FAMILY, CANNOT BE DISULFIDE-LINKED (BY
                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                         318
453
453
450
450
163
236
255
269
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337
453 AA;
                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                               381 CKGDC 385
                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CRGDC 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY)
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                                                                                                                                                                                                                                                                                                                                                 CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                                                                                   CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                      DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     СDF9 НС
060383;
                                                                                                                                                                                                                                                         PROPEP
                                                                                                                                                                                                                                                                      CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GDF9_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this etatement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BIOL. Reprod. 60:381-386(1999).
-1- FUNCTION: REQUIRED FOR OVARIAN FOLLICULOGENESIS.
-1- SUBUNIT: HOMODIMER OR HETERODIMER (POTENTIAL). BUT, IN CONTRAST TO
         J. Biol. Chem. 268:3444-3449(1993).
-!- FUNCTION: REQUIRED FOR OVARIAN FOLLICULOGENESIS.
-!- SUBUNIT: HOMODIMER OR HETERODIMER (FOTENTIAL). BUT, IN CONTRAST TO OTHER MEMBERS OF THIS FAMILY, CANNOT BE DISULPIDE-LINKED.
-!- TISSUE SPECIFICITY: OVARY.
-!- SIMILARITY: Belongs to the TGF-beta family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDINES 1916005, BOGENESSINE T.Y.; BOGENESINE K.J.; Clay C.M., Moeller C.L., Sawyer H.R.; Bodensteiner K.J.; Clay C.M., Moeller C.L., Sawyer H.R.; Molecular cloning of the ovine Growth/Differentiation factor-9 gene and expression of growth/differentiation factor-9 in ovine and bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
factor-beta superfamily containing a novel pattern of cysteines.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Caprinae; Ovis.
                                                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                          POTENTIAL.
GROWTH/DIFFERENTIATION FACTOR 9.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. ..) (POTENTIALINED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 32; DB 1; Length 441;
Pred. No. 42;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                      N-LINKED (GLCNAC. . .) (PO
N-LINKED (GLCNAC. . .) (PO
E27071359B899C3C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GDF9 SHEEP STANDARD, PRT; 453 AA. 077681; 30-MAY-2000 (Rel. 39, Created) 30-MAY-2000 (Rel. 39, Last sequence update) 28-FRB-2003 (Rel. 41, Last annotation update) Growth/differentiation factor 9 precursor (GDF-9).
                                                                                                                                                                                                                                                       PRINTS; PRO0669; INHIBINA.
Prodom; PD000357; TGFb; 1.
SMART; SM00204; TGFB; 1.
GROSTER; PS500250; TGF BETA 1; 1.
Growth factor; Cytokine; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                   POTENTIAL.
                                                                                                                                                                                                            MGD; MGI:95692; Gdf9.
InterPro; IPR0024065; Inhibin_alpha.
InterPro; IPR001839; TGFb.
Pfam; PF00019; TGF-beta; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                               49636 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    91.4%;
80.0%;
                                                                                                                                                                              EMBL; L06444; AAA53035.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Conservative
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2229
2229
                                                                                                                                                                                        S45284; S45284.
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Best Local Similarity
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369 CKGDC 373
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DISULFID
DISULFID
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Kimmerly W., Bondoc M., Cheng J., Connolly K.S., Gunning K.M.,
Davis C.A., Kadner K., Miguel T., Pitluck S., Pollard M., Rojeski
Subramanian S., Martin C.H.,
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
--- FUNCTION: REQUIRED FOR OVARIAN FOLLICULOGENESIS.
--- SUBUNIT: HOMODIMER OR HETERODIMER (POTENTIAL). BUT, IN CONTRAS.
OTHER MEMBERS OF THIS FAMILY, CANNOT BE DISULFIDE-LINKED (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
GROWTH/DIFFERENTIATION FACTOR 9.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N'LINKED (GLCNAC. .) (POTENTIAL)
N'LINKED (GLCNAC. .) (POTENTIAL)
N'LINKED (GLCNAC. .) (POTENTIAL)
N'LINKED (GLCNAC. .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91.4%; Score 32; DB 1; Length 453; 80.0%; Pred. No. 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1911A66A720E2B85 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-UUL-1999 (Rel. 38, Created)
15-UUL-1999 (Rel. 38, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Grow-Ndifferentiation factor 9 precursor (GDF-9).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY).
-!- SIMILARITY: Belongs to the TGF-beta family.
SIMILARITY).
SIMILARITY: Belongs to the TGF-beta family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00204; TGFB; 1.
PROSITE; PS00250; TGF BETA 1; 1.
Growth factor; Cytokine; Glycoprotein; Signal. SIGNAL 1.
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InterPro; IPR002405; Inhibin_alpha.
InterPro; IPR001839; TGPb.
InterPro; IPR001839; TGF-beta; 1.
PR.INTS; PR00669; INHIBINA.
PRODOM; PD000357; TGFb; 1.
                                                                                                                                                                                                                                                                                                                                            EMBL; AF078545; AAC28089.2; -.
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SIGNAL PROPEP

DOMAIN CHAIN

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                                                                                                                                                                                                                                                                                                                                                                                                                                             INDUCTION: By cadmium.

DOMAIN: ALL CYSTEINE RESIDUES ARE ARRANGED IN C-X-C GROUPS. THESE ARE THOUGHT TO BE THE METAL-BINDING SITES IN OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SIMILARITY: BELONGS TO THE METALLOTHIONEIN SUPERFAMILY; FAMILY 6.
                                                                                                                                                                                       Kugawa F., Yamamoto H., Osada S., Aoki M., Imagawa M., Nishihara T., "Metallothionein genes in the nematode Caenorinabditis elegans and metal inducibility in mammalian culture cells.";
Biomed. Brviron. Sci. 7:222-231(1994).
       Freedman J.H., Slice L.W., Dixon D., Fire A., Rubin C.S.;
"The novel metallothionain genes of Caenorhabditis elegans.
"Extructural organization and inducible, cell-specific expression.";
J. Biol. Chem. 268:2554-2564(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                STRAIN=Bristol N2; Greco T., Bradshaw H.; Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases. Submitted THIS PROTEIN BINDS CATIONS OF SEVERAL TRANSITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=93155193; PubMed=8429021; McPherron A.C., Lee S.-J.; "GDF-3 and GDF-9: two new members of the transforming growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             D -> G (IN REF. 2; AA SEQUENCE)
DA0D00C9FD6240C3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91.4%; Score 32; DB 1; Length 74; 80.0%; Pred. No. 8.4; cive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M92909; AAA28110.1; -.
EMBL; X52244; CAA37334.1; -.
EMBL; D17364; BAA04180.1; -.
EMBL; U64853; AAB04979.1; -.
PIR; B45206; B45206.
Wormbep; K11G9.4; CR0739.
InterPro; IRO00853; M11thion_nemat.
PRINTS; PRO0876; MIYEMATODE.
Metal_binding; Metal_thiolate cluster; Cadmium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-0CT-1994 (Rel. 30, Created)
01-0CT-1994 (Rel. 30, Last sequence update)
28-FBE-2003 (Rel. 41, Last annotation update)
Growth/differentiation factor 9 precursor (GDF-9)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           441 AA.
                                                                                                                   SEQUENCE FROM N.A.
STRAIN-Bristol N2;
MEDLINE-95151184; PubMed=7848551;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22 22
74 AA; 7959 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 80.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     METALLOTHIONEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse)
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Q07105;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=90094407; PubMed=2294106;
Slice L.W., Freedman J.H., Rubin C.S.,
"Purification, characterization, and cDNA cloning of a novel
metallothionein-like, cadmium-binding protein from Caenorhabditis
                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL)
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Pred. No. 23;
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01-AUG-1990 (Rel. 15, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
MTL-1 OR MET-1 OR K11G9.6.
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ARG-RICH.
BY SIMILARITY.
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                                                                                                                                                                                            POTENTIAL
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Biochem. J. 268:237-240(1990).
InterPro; IPR001839; TGFb.
PFam, PF00019; TGF-beta; 1.
PRINTS; PR00669; INTELINA.
ProDom; PD000357; TGFb; 1.
SMART; SW00204; TGFB; 1.
Growth factor; GlycopTotein; Sign.
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MEDLINE-90262552; PubMed=2344361;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     elegans.";
J. Biol. Chem. 265:256-263(1990)
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CARBOHYD

Best Loc Matches

RESULT 3

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RATAIL NEEDENTRELEY,

RATAIL NEEDENTRELEY,

RATAIL Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Admaratides P.G., Scherer S.E., Lin P.W., Hookins R.A., Galle R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Bradon R.C., Rogers Y.-H.C., Blazel R.G., Champpe M., Pfeiffer B.D.,

RA Bardon R.C., Rogers Y.-H.C., Blazel R.G., Mallon C.R., Miklos G.L.G.,

RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA Barlew R.M., Basu A., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

RA Burtis K.C., Busam D.A., Burlar H., Cadieu E., Certer A., Chandra I.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

RA Borkova D., Botchan M.R., Bullar H., Cadieu E., Certer A., Chandra I.,

RA Gorge K., Doup L.E., Downes M., Dugan Rochas S., Dunkov B.C., Dunn P.,

RA Durbin K.J., Evangelista C.C., Mays A.D., Dew I., Dietz S.M.,

RA Godson K., Doup L.E., Downes M., Dugan Rochas S., Dunkov B.C., Dunn P.,

RA Harris N.L., Harvey D.A., Herman T.J., Herniedz J.R., Houck J.,

RA Hostin D., Houston K.A., Howland T.J., Wei M. H., Ibegwam C.,

A Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A.,

RA Hostin D., Houston K.A., Howland T.J., Wei M. H., Ibegwam C.,

A Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,

RA Martei B. M., Morphy B., Murphy B., Murphy D.M., Norherson D.L.,

RA Merkulov G., Milshina N.V., Mobarry C., Morels J., Moshrefi A.,

RA Mount S.M., Noy M., Nurphy B., Nurshy D.M., Nelson D.L.,

RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Person D.D.,

RA Nelson D.R., Nixon K., Nusskern D.R., Person D.D.,

RA Nelson D.R., Nixon K., Nusskern D.R., Person D.D.,

Radoms K. Willer R.D., Nixon R., Nusskern D.R., Person D.D.,

Radoms K. Willer R.D., Nixon R., Nusskern D.R., Person D.D.,

Radoms K. Willer R.D., Respective M. Wurphy B., Nusskern D.R.,

Radoms K. Willer R.D., Nixon R., Nusskern D.R., Person D.D.,

Radoms K. Willer R.D., Respec
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                                                                                                                   DAUER LARVA DEVELOPMENT REGULATORY GROWTH
                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                      ID IHB_DROME STANDARD; PRT; 946 AA.

AC 061643; QBWRB1; QBWR60; Q9V497;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-CCT-2003 (Rel. 42, Last sequence update)
DT 10-CCT-2003 (Rel. 42, Last amocation update)
DT 10-CCT-2003 (Rel. 42, Last amocation update)
SE Inhibin beta chain precursor (Activin beta chain).
S Drosophila melanogaster (Fruit fly).
C Enkaryota; Metazoda; Arthropda; Haxapoda; Insecta; Pterygota;
C Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
C Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                            BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
N.LINKED (GLONAC. .) (POTENTIAL).
B.-SI IN B1372; LOSS OF FUNCTION.
G->R: IN M70; LOSS OF FUNCTION.
                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                        (POTENTIAL)
                                                                                                                                                                                                                                                                                               100.0%; Score 35; DB 1; Length 350; 100.0%; Pred. No. 9.5; ive 0; Mismatches 0; IndelB
                                                                        protein; Glycoprotein; Signal
                                                                                                                                                                                                                                                                   F957C70A2B1FDE0A CRC64;
                                                                                                                                 FACTOR DAF-7
Pfam; PF00019; TGF-beta; 1.
PRINTS; PR00439; GFCYSKNOT.
ProDom; PD000357; TGF9; 1.
SMART; SM00204; TGFB; 1.
PROSITE; PS00250; TGF BETA 1; 1.
Growth factor; Developmental prote SIGNAL
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23 27
271 2
280 2
350 AA;
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235
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CARBOHYD
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation — the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
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SEQUENCE FROM N.A.
STRAIN=Berkeley; TISSUE=Embryo;
MEDLINE=22426066, PubMed=12537569;
Stapleton M., Carlson J.W., Broketein P., Yu C., Champe M.,
George R.A., Gharin H., Kronmiller B., Pacleb J.M., Park S., Wan K.H.,
Rubin G.M., Celniker S.E.;
"A brosophila full-length CDNA resource.";
Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8
Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Shenett K., Sanders R.D.C., Scheeler F., Shen H., Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Spier B., Spradling A.C., Stapleton M., Skupski M.P., Smith T., Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang S.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodey T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zhong F.W., Zhong W., Zhou W., Zhu S., Smith H.O., Gibbs R.A., Myers B.W., Rubin G.M., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIINE=22426069; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
Bettencourt B.R., Celniker S.E., de Grey A.D. M.J., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lewis S.E.;
"Annotation of the Drosophila melanogaster euchromatic genome:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    systematic review.";
Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
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EMBL; AF454392; AAL51005.1; --.
EMBL; AF054822; AAC39083.1; --.
HSSP, 18075; 1BMP.
FlyBase: FEgn0024913; activin-beta.
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TISSUE=Embryo;
MEDLINE=22090541; PubMed=12095682;
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WormPep; B0412.2; CE01758.
InterPro; IPR002400; GF cysknot.
InterPro; IPR001839; TGPb.
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EMBL, U72884; AAC47389.1; -.
EMBL, U80053; AAB52554.1; -.
PIR; T25451; T35451.
HSSP; P12643; 3BMP.
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P92172;
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salmo salar
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                  5.1.6
Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             141681 segs, 52070155 residues
                     version 5 - 2004 (
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GDF9_MOUSE
GDF9_HWAN
BGLK_ERWCH
TRR1_SALGA
TRR2_SALGA
POLS_EEEVVB
POLS_EEEVVB
POLS_EEVVB
POLS_EEVVB
POLS_EEVVB
POLS_EEVVB
POLS_EEVVB
POLS_EEVVB
POLS_EEVVB
VLT_EVVB
POLS_EEVVB
VLT_EVVB
VLT_EVV
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GUN4_TRIRE
BMP4_XENLA
BMP4_CHICK
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                   protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                               BLOSUM62
Gapop 10.0 , Gapext 0.5
                     GenCore (c) 1993
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Maximum DB seq length: 2000000000
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35
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Match Length
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Perfect score:
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                                                                                                                   OM protein -
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                  046576 oryctolagus
P14000 hemicentrot
P50473 strongyloce
P27738 apple chlor
P5491 apple chlor
P5918 conus catus
P83627 armadillidi
                                                   homo sapien
                                                                                                      mus musculu
rattus norv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    THENDER SPECIFICITY: EXPRESSION in the chemosensory neurons.
DEVELOPMENTAL STAGE: WHEN THE FOOD/PHEROMONE RATIO IS HIGH, ITS
LEVEL PERKS DURING THE L1 LARVAL STAGE. EXPRESSION IS DETECTED IN
LARVAE BEGINNING 4 TO 5 HOURS AFTER HATCHING, THROUGH THE FOUR
LARVAE STAGES, AND IN ADULTS.
INDUCTION: Dauge-1-inducing pheromone inhibits its expression and
promotes dauger formation, whereas food reactivates its expression
and promotes recovery from the dauger state.
SIMILARITY: Belongs to the TGF-beta family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
10-OCT-2003 (Rel. 42, Last amortation update)
10-OCT-2003 (Rel. 42, Last amortation update)
10-OCT-2003 (Rel. 42, Last amortation protein 7)
11-OCT-2003 (Rel. 42, Last amortation protein 7)
12-OCT-2003 (Rel. 42, Last amortation protein 7)
13-OCT-2003 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-Bristol N2;
MEDLINE-97067238; PubMed-8910282;
RCD F., Lim C.-S., Johnsen R., Albert P.S., Pilgrim D., Riddle D.L.;
RCONTrol of C. elegans larval development by neuronal expression of a TGF-beta homolog.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bentley D.;
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: May act as a negative regulator of dauer larva
development by transducing chemosensory information from ASI
                                                                                                 P21275
Q06826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  350 AA
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                                        BMP4_HUMAN
BMP4_MOUSE
BMP4_RAT
BMP4_RABIT
ARS_HEMPU
ARS_STRPU
                                                                                                                                                                                                                                                                                                                       MUSA_HUMAN
RRPO_ACLSP
RRPO_ACLSA
CXOB_CONCT
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11885
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genome polyprotein - eastern equine encephalomyelitis virus
N;Contains: 6K protein; capsid protein C; envelope protein E1; envelope protein E2; envel
C;Species: eastern equine encephalomyelitis virus
C;Date: 06-Jan-1994 #sequence_revision 01-Nov-1996 #text_change 26-Aug-1999
C;Accession: S26373
R;Volchkov, V.E.; Volchkova, V.A.; Netesov, S.V.
Mol. Gen. Mikrobiol. Virusol. 5, 8-15, 1991
A;Fitle: Complete nucleotide sequence of the eastern equine encephalomyelitis virus genom A;Reference number: S26369; MUID:91375524; PMID:1896061
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N;Contains: 6K protein; capsid protein; El protein; E2 potein; E3 protein
C;Species: eastern equine encephalomyelitis virus
C;Species: eastern equine encephalomyelitis virus
C;Accession: 0.4 May-1998 #sequence_revision 15-May-1998 #text_change 26-Aug-1999
C;Accession: S72350
R;Weaver, S.C.; Hagenbaugh, A.; Bellew, L.A.; Netesov, S.V.; Volchkov, V.E.; Chang, G.J.:
Viroloyy 197, 375-390, 1993
A;Title: A comparison of the nucleotide sequences of eastern and western equine encephalc
A;Reference number: S72349; MuID:94025587; PMID:8105605
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A, Residues: 1-1241 «VOL»
A, Residues: 1-1241 (VOL»
A, Residues: 1-1241 (VOL»
A, Cross-references: EMBL.X63135; NID:959185; PIDN:CAA44845.1; PID:959186
A, Residuece could not be checked because of bad print in paper
A, Rote: sequence could not be checked because of bad print in paper
C, Superfamily: Logavirus structural polyprotein
C, Superfamily: Logavirus structural polyprotein
F, 1260/Product: capsid protein C #status predicted (CAP»
F, 261-232/Product: envelope protein E3 #status predicted (EB2»
F, 324-743/Product: envelope protein E2 #status predicted (EP2»
F, 744-800/Product: structural #status predicted (EP2»
F, 801-1241/Product: envelope protein E1 #status predicted (EP2»
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Pred. No. 2.3e+02;
1; Mismatches 0; Indels
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Pred. No. 2.3e+02;
1; Mismatches 0;
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les 4; Conservative
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Best Local Similarity
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1 CRGDC 5
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                                                                           structural polyprotein - eastern equine encephalomyelitis virus (strain 82V-2137)
N;Contains: 6K protein; coat protein C; membrane glycoprotein E1; membrane glycoprotein
N;Contains: 6K protein; coat protein C; membrane glycoprotein E1; membrane glycoprotein
C;Species: astern equine encephalomyelitis virus
C;Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 16-Jul-1999
C;Accession: A26816
R;Chang, G.J.J; Trent, D.W.
J; Gardy, G.J.J; Trent, D.W.
J; Gardy, G.J.J; Trent, D.W.
A;Title: Nucleotide sequence of the genome region encoding the 26S mRNA of eastern equin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              structural polyprotein - eastern equine encephalomyelitis virus (strain VA33[Ten Broeck] N;Contains: 6K protein; coat protein C; membrane glycoprotein E1; membrane glycoprotein C;Species eastern equine encephalomyelitis virus A;Note: host Equus caballus (domestic horse) C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 16-Jul-1999 C;Accession: A39992
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A/Mocessian A3240 WEA
A/Rossian A3240 WEA
A/Rossian A3240 WEA
A/Rossian A3240 WEA
A/Rossian A3240 WEA
A/Moces the authors translated the codon AGC for residue 836 as Arg and GUU for residue C;Superfamily: togavirus structural polyprotein
C;Superfamily: togavirus structural polyprotein
C;Superfamily: togavirus structural polyprotein
E/1-260/Product: coat protein; Glycoprotein; polyprotein; transmembrane protein
E/1-260/Product: membrane glycoprotein E3 #status predicted <EG3>
F/324-743/Product: membrane glycoprotein E3 #status predicted <EG3>
F/695-712/Domain: transmembrane #status predicted <TM2>
F/324-743/Product: membrane #status predicted <TM3>
F/324-743/Product: membrane #status predicted <TM3>
F/324-743/Product: wealver #status predicted <TM3>
F/324-743/Product: wealver #status predicted <TM3>
F/32-748/Domain: transmembrane #status predicted <TM3>
F/32-
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Virology 182, 774-784, 1991
A;Title: Molecular evolution of eastern equine encephalomyelitis virus in North America.
A;Reference number: A39992; MUID:91220727; PMID:2024496
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F;781-799/Domain: transmembrane #status predicted <TM4>
F;781-799/Domain: transmembrane #status predicted <TM4>
F;800-1240/Product: membrane glycoprotein E1 #status predicted <EG1>
F;1212-1236/Domain: transmembrane #status predicted <TM5>
F;49,271,625,638,834,933/Binding site: carbohydrate (Asn) (covalent) #status predicted
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F;777-798/Domain: transmembrane glycoprotein El #status predicted <MGl>
F;1211-1255/Domain: transmembrane #status predicted <TN5>
F;49,270,624,637,932/Binding Bite: carbohydrate (Asn) (covalent) #status predicted
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A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1.1239 ccHA
A; Cross-references: EMBL:X05816; NID:g62074; PIDN:CAA29261.1; PID:g62075
C; Superfamily: togavirus structural polyprotein
C; Reywords: coat protein; glycoprotein; transmembrane protein
F; 259, Product: coat protein C #status predicted cCPC>
F; 260-322/Product: membrane #status predicted cTN1>
F; 251-277/Domain: transmembrane #status predicted cTN2>
F; 644-701/Domain: transmembrane #status predicted cTN2>
F; 647-737/Domain: transmembrane #status predicted cTN2>
F; 777-737/Domain: transmembrane #status predicted cTN3>
F; 777-737/Domain: transmembrane #status predicted cTN2>
F; 777-737/Domain: transmembrane #status predicted cTN3>
F; 777-737/Domain: transmembrane #status
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Pred. No. 2.3e+02;
1; Mismatches 0;
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80.0%;
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Best Local Similarity 80.0.
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Length 1242; Indels

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transferrin - Atlantic salmon
CiSpecies: Salmo salar (Atlantic salmon)
CiSpecies: Salmo salar (Atlantic salmon)
CiAccession: T11749
Mol. Marine Biol. Blocechnol. 2, 233-238, 1993
A;Title: Cloning and characterization of Atlantic salmon (Salmo salar) serum transferrin
A;Reference number: Z1732; MUID:94122797; PMID:8293074
A;Accession: T11749
A;Accession: T11749
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-690 <KVI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein C34G6.6 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C;Accession: C87789
R;anonymous, The C. elegans Sequencing Consortium.
Scrience 282, 2012-2018, 1998
A;Aritle: Genome sequence of the nematode C. elegans: a platform for investigating biology
A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www sanger.ac.uk/Projects/C_elegans/A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
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A.Experimental source: liver
C.Superfamily: transferrin; transferrin repeat homology
C.Keywords: iron binding
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80.0%; Pred. No. 2e+02;
ive 1; Mismatches 0; Indels
                                                                                                                                                                                                         Length 654;
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91.4%; Score 32; DB 2; Length 690;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                             0; Indels
                           A; Reference number: S53805; MUID:95198684; PMID:7891660
                                                                                                                                                                                                   Score 32; DB 2; 1
Pred. No. 1.4e+02;
1; Mismatches 0;
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80.0%; Pre
tive 1;
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Matches 4; Conservative
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Best Local Similarity 80.0
Matches 4; Conservative
                                                         A,Accession: S53805
A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-654 <VRO>
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A; Residues: 1-1011 <STO>
                                                                                                                                                                                                                                                                                                                                                                      367 CKGDC 371
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186 CKGDC 190
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A;Gene: C34G6.6
A;Map position: 1
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                           C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Date: 16-Peb-2001 #sequence_revision 16-Peb-2001 #text_change 16-Peb-2001
C.Date: 16-Peb-2001 #sequence_revision 16-Peb-2001 #text_change 16-Peb-2001
R.Ancession: D85098
R.Ancession: D85098
A.Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A.Accession: D85098
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A, Residues: 1-441 <INC>
A, Cross-references: EMBL:X77112
A, Experimental source: overy, strain 129SvEv (Stratagene)
R, McPhertron, A.C.; Lee, S.J.
J. Biol. Chem. 268, 3444-3449, 1993
A, Title: GDF-3 and GDF-9: two new members of the transforming growth factor-beta superfa
A, Reference number: A46607; MUID:93155193; PMID:8429021
A, Molecule type: mRNN
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C;Date: 27-Oct-1995 #sequence_revision 27-Feb-1997 #text_change 13-Mar-1997
C;Accession: S53805
R;Vroemen, S:; Heldens, J.; Boyd, C.; Henrissat, B.; Keen, N.T.
Mol. Gen. Genet. 246, 465-477, 1995
A;Title: Cloning and characterization of the bgxA gene from Erwinia chrysanthemi D1 whid
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A;Residues: 1-210 <STO>
A;Cross-references: GB:NC_001268; NID:g7267657; PIDN:CAB78085.1; GSPDB:GN00140
C;Genetics:
A;Gene: A;4909620
A;Map position: 4
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A;Residues: 1-295,'T',297-441 <MCP>
A;Cross-references: GB:L06444; NID:g293348; PIDN:AAA53035.1; PID:g567206
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hypothetical protein AT4g09620 [imported] - Arabidopsis thaliana
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Pred. No. 1e+02;
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C,Genetics:
A,Introns: 133/1
C,Superfamily: inhibin
C,Keywords: growth factor; ovary
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Best Local Similarity 80.0
Matches 4; Conservative
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Matches 4; Conservative
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Best Local Similarity 100. Matches 5; Conservative

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C;Accession: T48370
R;Bevan, M.; Pohl, T.; Weizenegger, T.; Bancroft, I.; Mewes, H.W.; Rudd, S.; Lemcke, K.; submitted to the Protein Sequence Database, March 2000
A;Reference number: Z24492
A;Accession: T48370
A;Attus: preliminary
A;Molecule type: DNA
A;Residues: 1-132 <BEV>
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R; Weaver, S.C.; Bellew, L.A.; Gousset, L.; Repik, P.M.; Scott, T.W.; Holland, J.J.
Virology 195, 700-709, 1993
A;Title: Diversity within natural populations of eastern equine encephalomyelitis virus.
A;Reference number: A48608; MUID:93331728; PMID:8101674
A;Contents: 215-85, MD85B
A;Accession: A48608
A;A
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Species: Arabidopsis thaliana (mouse-ear cress)
Pate: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 28-Jul-2000
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C,Species: eastern equine encephalomyelitis virus
C,Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 26-Aug-1999
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A;Residues: 1-207 <WEA>
A;Cross-references: GB:S63996; NID:9400551, PIDN:AAB27576.1; PID:9400552
A;Note: sequence extracted from NCBI backbone (NCBIN:135481, NCBIP:135482)
C;Superfamily: togavirus structural polyprotein
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A;Note: F12E4.220
C;Superfamily: Arabidopsis thaliana hypothetical protein F12E4.220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 32; DB 2; Length 132;
Pred. No. 40;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91.4%; Score 32; DB 2; Length 207;
80.0%; Pred. No. 57;
tive 1; Mismatches 0; Indels
                                                                                                                               Score 32; DB 2; Length 75;
Pred. No. 26;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Cross-references: EMBL:AL162751
A;Experimental source: cultivar Columbia; BAC clone F12E4
C,Genetics:
                                                                                                                          91.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         th 91.4%;
Similarity 80.0%;
4; Conservative
A;Introns: 6/1
C;Superfamily: metallothionein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein F12E4.220
                                                                                           4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
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Best Local Similarity
Matches 4; Conserv
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A, Readdues: 1-75 eKRS
A, Note: sequence extracted from NCBI backbone (NCBIP:124147)
R; Imagawa, M; Onozawa, T.; Okumura, K; Osada, S.; Nishihara, T.; Kondo, M.
Biochem, J. 268, 237-240, 1990
A; Title: Characterization of metallothionein cDNAs induced by cadmium in the nematode
A, Reference number: S09714; MUID:90262552; PMID:2344361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Gene: CESP:W01C8.3
A;Introns: 59/3; 92/2; 157/3; 189/3; 220/2; 251/3; 275/2; 319/1; 374/3; 407/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein W01C8.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T26044
R;Nhan, M.
                                                   Gaps
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A; Residues: 1:75 < IMA>
A; Residues: 1:75 < IMA>
A; Cross-references: EMBL:X53244; NID:g6779; PIDN:CAA37334.1; PID:g6780
R; Greco, T.; Bradshaw, H.
R; Greco, T.; Bradshaw, H.
Bubmitted to the EMBL Data Library, July 1996
A; Description: The sequence of C. elegans cosmid K11G9.
A; Reference number: Z20672.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Status: preliminary; not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A, Residues: 1-1076 <NHA>
A, Cross-references: EMBL:U41509; PIDN:AAA82623.1; CESP:W01C8.3
                                                   Indels
                                                   .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                submitted to the EMBL Data Library, November 1995
A; Description: The sequence of C. elegans cosmid W01C8.
A; Reference number: Z20142
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A;Molecule type: DNA
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metallothionein 2 - Caenorhabditis elegans

A; Molecule type: DNA A; Residues: 1-75 <GRE>

A; Accession: T29721

A; Accession: S09714

Gene: CESP:K11G9.6

Genetics:

A; Map position: 5

Best Local Similarity Matches 5; Conserv

Query Match

C, Genetics:

A; Accession: T26044

278 CRGDC 282

1 CRGDC 5

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

September 22, 2004, 06:46:27; Search time 39 Seconds (without alignments) 12.332 Million cell updates/sec Run on:

US-09-912-609-9 35

1 CRGDC 5 Title: Perfect score: Seguence: Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283366

283366 seqs, 96191526 residues

Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

IES	scri		activin - fruit f	hynotherical-prote	metallothionein o	hypothetical prote	7.5			beta-qlucosidase/<	transferrin - Arla	'n	Structural polymo		Genome nolymenter	atmictinal polimen	structural polypr	structural polypro			٠.		Structural polypro	. "	, ,-	٠.	hymothetical prote	probable olicens	type IV president	F19K19.12 protein
SUMMARIES	ID	T25451	PW0042	T26044	B45206	T48370	A48608	D85098	S45284	S53805	T11749	C87789	VHWVEE	VHWVEV	\$26373	872350	A56605	VHWVVE	VHWVVT	JQ1978	JQ1979	B44213	D44213	T30075	T30074	E83128	A96544	F71545	847153	8630
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	Length	350	373	1076	75	132	207	210	441	654	069	101	1239	1240	1241	1242	1242	1254	1254	1254	1254	1255	1255	2090	2153	80	154	247	249	342
de	Query	100.0	100.0	100.0	91.4	91.4	91.4	91.4	91.4	91.4	91.4	91.4	91.4	91.4	91.4	91.4	91.4	91.4	91.4	91.4	91.4	91.4	91.4		91.4	88.6	88.6	88.6		88.6
	Score	35	35	35	32	32	32	32	32	32	32	32	32	32	32	32	32	32	32	32	32	32	32	32	32	31	31	31	31	31
	Result No.	-	N	e	4	ស	φ	7	œ	თ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

cell wall glycopro	hypothetical prote	S-receptor kinase	Acorf-117 protein	ACMNPV orf117 - Bo	inhibin beta-A cha	E7 protein - human		profein -		orotein -	orotein - 1	protein	ivin hera	19.3 (impo
\$50062	A12893	T00534	F72864	T41855	A36192	S36492	S36486	W7WL8	W7WL47	W7WL5	W7WLB5	836539	PN0504	C96559
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88.6	88.6	88.6	85.7	85.7	85.7	85.7	85.7	85.7	85.7	85.7	85.7	85.7	85.7	85.7
31	31	31	30	30	30	30	30	30	30	30	30	30	30	30
30	3 C	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

transfor	transforming growth factor beta homolog - Caenorhabditis elegans C;Species: Caenorhabditis elegans
C; Date:	C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 17-Mar-2000
R; Bentley	R;Bentley, D.
submitte A;Descrit	to the EMBL Data Library, December 1996 tion: The sequence of C. elegans cosmid R0412
A, Refere	A, Reference number: Z20037
A; Access:	A; Accession: T25451
A;Status A;Molecu]	A;Scacus: preliminary; cranslated from GB/EMBL/DDBJ A;Molecule type: DNA
A; Residue	A; Residues: 1-350 < BEN>
A;Cross-1	eferences: EMBL:U80953; PIDN:AAB52554.1; GSPDB:GN00021
A; Experin	A; Experimental source: strain Bristol N2; clone B0412
C;Generics: A:Gener daf-7	
A; Map position: 3	ition: 3
A; Introns C; Superfa	A;Introns: 43/3; 123/3; 184/2; 288/3 C;Superfamily: inhibin
Query Match Best Local	Query Match 100.0%; Score 35; DB 2; Length 350; Best Local Similarity 100 0%: Dred No 24:
Matches	#
٥'n	1 CRGDC 5
Db	278 CRGDC 282

duction - Intuit ity (Urosphila sp.) (tragment)

C.Specides: Drosophila sp.) (tragment)

C.Specides: Drosophila sp.)

C.Date: 18-Jun-1998 #sequence\_revision 10-Jul-1998 #text\_change 17-Nov-2000

C.Accession: PW0042

B.Kutty, G.; Kutty, R.K.; Samuel, W.; Duncan, T.; Jaworski, C.; Wiggert, B.

B.Kutty, G.; Kutty, R.K.; Samuel, W.; Duncan, T.; Jaworski, C.; Wiggert, B.

B.A.Ritle: Identification of a new member of transforming growth factor-beta superfamily in A.Recession: PW0042

A.Recession: PW0042

A.Accession: PW0042

A.Accession: PW0042

A.Residues: 1-373 «KUT>

A.Residues: 1-374 «KUT> activin - fruit fly (Drosophila sp.) (fragment)

100.0%; Score 35; DB 2; Length 373; Query Match

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74.3%; Score 26; DB 100.0%; Pred. No. 3e+tive 0; Mismatches
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TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                         Query Match 74.3
Best Local Similarity 100.
Matches 4; Conservative
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                                                                                                                                                                                                                                              Sequence 34, Application US/08753781C
| Patent No. 5951981
| GENERAL INFORMATION: | Francis S. |
| APPLICANT: Bush, Larry R. |
| APPLICANT: Bush, Larry R. |
| APPLICANT: Swenson, Stephen |
| APPLICANT: Swenson, Stephen |
| APPLICANT: Flores Sanchez, Eladio |
| TITLE OF INVENTION: THROMBOLYTIC AGENTS WITH ANTITHROMBOTIC ACTIVITY |
| FILE REPERBENCE: DIT1 124 |
| CURRENT APPLICATION NUMBER: US/08/753,781C |
| CURRENT FILING DATE: 1996-12-02 |
| NUMBER OF SEQ ID NOS: 40 |
| SEQ ID NO 34 |
| LENGTH: 4 |
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                                    Query Match 74.3%; Score 26; DB 2; Length 4; Best Local Similarity 100.0%; Pred. No. 38+05; Matches 4; Conservative 0; Mismatches 0; Indels
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3e+05;
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100.0%; Pred. No. co.
0; Mismatches
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LOCATION: (1)
OTHER INFORMATION: ACETYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
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NAME/KEY: MOD_RES
LOCATION: (4)
OTHER INFORMATION: AMIDATION
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Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                   2 RGDC 5
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APPLICANT: Dean, Richard T.
APPLICANT: Lister-James, John
TITLE OF INVENTION: THROMBUS IMAGING AGENTS
FILE REFERENCE: DITI 113.1USC1
CURRENT APPLICATION NUMBER: US/09/141,127A
CURRENT FILING DATE: 1998-08-27
EARLIER FILING DATE: 1998-01-05
EARLIER APPLICATION NUMBER: PCT/US93/04794
EARLIER PILING DATE: 1993-05-21
EARLIER FILING DATE: 1993-05-21
EARLIER FILING DATE: 1993-05-21
EARLIER FILING DATE: 1993-05-21

SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 14 LENGTH: 4

NUMBER OF SEQ ID NOS: 40

US-09-141-127-14
; Sequence 14, Application US/09141127A
; Patent No. 6083481
; GENERAL INFORMATION:

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                                                                                                                                                                                                                                        Gaps
NAME/KEY: MOD_RES
LOCATION: (1)
OTHER INFORMATION: ACETYLATION
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (4)
OTHER INFORMATION: AMIDATION
FEATURE:
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
OTHER INFORMATION: peptide
US-09-141-127-14
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                                                                                                                                                                                                     DB 3; Length 4; 3e+05;
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NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: /label= Acetyl
OTHER INFORMATION: /note= "The amino terminus is modified by covalent
OTHER INFORMATION: linkage to an acetyl group."
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= Amide
//note= "The carboxyl terminus is modified to an
amide=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 41, Application US/08335832
Patent No. 5925331
GENEAL INFORMATION:
APPLICANT: Dean, Richard T
APPLICANT: Lister-James, John
TITLE OF INVENTION: Technetium-99m Labeled Peptides for TITLE OF INVENTION: Thrombus Imaging
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Allegretti, Ltd.
                                                                                                                                                                                                                                                                                                                                                                     Query Match 74.3%; Score 26; DB 1; Length 4; Best Local Similarity 100.0%; Pred. No. 34+05; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                            LOCATION: 4
OTHER INFORMATION: /label= Modified-site
OTHER INFORMATION: /note= "Asp is Asp-penicillamine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURREBNY APPLICATION DATE:

FILING DATE: 05-JAN-1995

CLASSIFICATION NUMBER: US/08/335,832

FILING DATE: 05-JAN-1995

CLASSIFICATION NUMBER: 92,216-I

REGISTRATION NUMBER: 92,216-I

TELEPHONE: 312-715-1000

TELEPHONE: 312-715-1000

TELEPAX: 312-715-1000

TELEFAX: 310-221-5317

INFORMATION FOR SEQ ID NO: 41: SEQUENCE CHARACTERISTICS:

LENGTH: 4 amino acide

TOPOLOGY: linear

MOLECULE TYPE: peptide
                     PEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: /label= Modified-site
OTHER INFORMATION: /note= "Cys is Ac-Cys."
NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: Modified-site
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OTHER INFORMATION: /
OTHER INFORMATION: /
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STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CRGD 4
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US-08-457-753-4
; Sequence 4, Application US/0845753
; Sequence 4, Application US/0845753
; GENERAL INFORMATION:
APPLICANT: ANDERSON, DAVID C.
; TITLE OF INVENTION: HEMOGLOBINS AS DRUG DELIVERY AGENTS
; CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street, N.W., Suite 300
; STATE: D.C.
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                           Query Match 74.3%; Score 26; DB 1; Length 4; Best Local Similarity 100.0%; Pred. No. 34+05; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                              ; OTHER INFORMATION: /label= Modified-site
; OTHER INFORMATION: /note= "Asp is Asp-penicillamine"
US-08-240-711-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:

MEDIUM TESE: Floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
APPLICATION NUMBER: US 08/457,753
FILING DATE: 10-101-1994
APPLICATION NUMBER: PCT/US92/09713
FILING DATE: 06-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/789,177
FILING DATE: 08-NOV-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/789,179
FILING DATE: 08-NOV-1991
APPLICATION NUMBER: US 07/789,179
FILING DATE: 08-NOV-1991
APPLICATION NUMBER: US 07/789,179
FILING DATE: US 08-NOV-1991
APPLICATION NUMBER: US 08-NOV-1991
                                                   NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: /label= Modified-site
OTHER INFORMATION: /note= "Cys is Ac-Cys."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: COOPER, IVER P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: ANDE
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
                                                                                                                                                                                                   NAME/KEY: Modified-site LOCATION: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 248633
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 4 amino acids
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CRGD 4
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GENERAL INFORMATION:
APPLICANT: ANDERSON, DAVID C.
APPLICANT: MATHEWS, ANTHONY J.
TITLE OF INVENTION: HEMOGLOBINS AS DRUG DELIVERY AGENTS
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                        Length 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                      85.7%; Score 30; DB 4;
80.0%; Pred. No. 3e+05;
Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SSE: Browdy and Neimark
1: 419 Seventh Street, N.W., Suite 300
Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/240,711
PILING DATE: 12-UUL-1994
CLASSIFICATION NUMBER: US/08/240,711
PRICK APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/09713
FILING DATE: 06-NOV-1992
PRICK APPLICATION NUMBER: US 07/789,177
PILING DATE: 08-NOV-1991
PRICK APPLICATION NUMBER: US 07/789,177
PILING DATE: 08-NOV-1991
PRICK APPLICATION NUMBER: US 07/789,177
PILING DATE: 08-NOV-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: ANDERSON=5A TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                            OTHER INFORMATION: Synthetic construct
PRIOR APPLICATION NUMBER: 60/153,512
PRIOR FILING DATE: 1999-09-13
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin version 3.2
SEQ ID NO 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/08240711 Patent No. 5679777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28,005
                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
PEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               202-628-5197
202-737-3528
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                    4; Conservative
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NAME/KEY: misc feature

COTATION: (1)...(5)

OTHER INFORMATION: Cyclo
US-09-660-377A-11
                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                             1 CRGDC 5
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TOPOLOGY: lin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: D.C. COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET:
CITY: Wa
                                                                                                                                                                                                                                                                                                                                                                                    Matches
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Patent No. 6685914

GENERAL INFORMATION:
APPLICANT: Liu, Shuang

TITLE OF INVENTION: Macrocyclic Chelants For Metallopharmaceuticals
FILE REFERENCE: BMS-2207

CURRENT APPLICATION NUMBER: US/09/660,377A

CURRENT APPLICATION NUMBER: US/09/660,377A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5318899-77;
Patent No. 5318899
APPLICANT: SCARBOROUGH, ROBERT M.;WOLF, DAVID L.;CHARO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: PLATELET AGGREGATION INHIBITORS NUMBER OF SEQUENCES: 83
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/483,229
FILING DATE: 20-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 418,028
FILING DATE: 06-OCT-1989
APPLICATION NUMBER: 367,509
FILING DATE: 16-JUN-1989
                          SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/924,002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                   FILING DATE:
CLASSIPTCATION: 530

GLASSIPTCATION DATA:
APPLICATION NUMBER: US 08/625,695
FILING DATE: 03-APR-1996
FILING DATE: 11-MAR-1994
APPLICATION NUMBER: US 08/212,186
FILING DATE: 11-MAR-1994
ATTORNEY AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 14.815
REFERENCE/DOCKET NUMBER: P-LA 2748
TELEFORMINICATION INFORMATION:
TELEFORMINICATION INFORMATION:
TELEFORMINICATION S35-9949
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 32;
Pred. No.
                                                                                                                                                                                                                                                                                                                         P-LA 2748
        · OPERATING SYSTEM: PC-DOS/MS-DOS
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80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 amino acids
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GY: both
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Best Local Similarity
Matches 4; Conserv
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Best Local Similarity
Matches 5; Conserv
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US-09-660-377A-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
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Gaps

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) OTHER INFORMATION: Description of Artificial Sequence: synthetic US-09-141-127-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 35; DB 3; Length 5;
100.0%; Pred. No. 36+05;
Ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 10. Application US/08924002
Patent No. 6177542
GENERAL INFORMATION:
APPLICANT: Ruoslahti, Erkki I.
APPLICANT: Roislahti, Erkki I.
TITLE OF INVENTION: NOVEL INTECRIN-BINDING PEPTIDES
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AMERICAN CAMPBELLE Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; GENERAL INFURGANTION;
; APPLICANT: Dean, Richard T.
; APPLICANT: Dean, Richard John
TITLE OF INVENTION: THROMBUS IMAGING AGENTS
FILE REFERENCE: DITI 113.1050.
; CURRENT APPLICATION NUMBER: US/09/141,127A
CURRENT FILING DATE: 1998-08-27
; EARLIER FILING DATE: 1995-01-05
EARLIER FILING DATE: 1995-01-05
EARLIER FILING DATE: 1993-05-21
EARLIER FILING DATE: 1993-05-21
EARLIER FILING DATE: 1993-05-21
EARLIER PILING DATE: 1993-05-21
EARLIER PILING DATE: 1993-05-21
SARLIER PILING DATE: 1993-05-21
SARLIER PILING DATE: 1993-05-21
SARLIER PILING DATE: 1993-05-21
SARLIER PILING DATE: 1993-05-21
SOFTWARE: PAREIT VOE: 2.0
; SEQ ID NOS: 40
                                                                                                                                                                                                                                                                                                                                                                                                  KESULA ,
US-09-141-127-15
; Sequence 15, Application US/09141127A
: Patent No. 6083481
    TELEFAX: (619) 535-8949

FINFORMATION FOR SEQ ID NO: 37

SEQUENCE CHARACTERISTICS:

LENGTH: 5 amino acids

TYPE: amino acids

TYPE: amino acids

TYPE: acids

TYPE: acids

TYPE: acids

TYPE: acids

TYPE: acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                     Ouery Match 100.
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100..
                                                                                                                                                                                                                                                                           1 CRGDC 5
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                                                                                                                                        US-08-286-861-37
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                                                                                                                                               Sequence 35, Application US/08753781C

Sequence 35, Application US/08753781C

Sequence 35, Application US/08753781C

Setting Reneral Processing State of Section State of TITLE OF INVENTION THROMBOLYTIC AGENTS WITH ANTITHROMBOTIC ACTIVITY CURRENT PELIGE REFERENCE: DITI 124

STILE REPERENCE: DITI 124

CURRENT PELING DATE: 1996-12-02

NUMBER OF SEQ ID NOS: 40

SEQ ID NO 35

LENGTH: 5

TYPE: PRT

CORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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OTHER INFORMATION: Description of Artificial Sequence:synthetic

OTHER INFORMATION: peptide
US-08-753-781-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Ruoslahti, Erkki
APPLICANT: Roslahti, Erkki
TITLE OF INVENTION: No. 5981478el Integrin-Binding Peptides
CORRESPONDENCE 46
CORRESPONDENCE ADDRESS:
ADDRESSE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 35; DB 2; Length 5; 100.0%; Pred. No. 38+05; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER PADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATURG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/286,861
FILING DATE: 04-AUG-1994
FLING PAPPLICATION DATA:
APPLICATION NUMBER: US 08/158,001
FILING DATE: 24-NOV-1993
ATTONENY/AGERT INFORMATION:
NAME: Camballor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: Campbell and Flores
4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Campbell, Cathryn
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LA 9992
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 37, Application US/08286861
Patent No. 5981478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 5, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: San Diego
STATE: California
COUNTRY: USA
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                                                                                                         RESULT 5
US-08-753-781-35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Dean, Richard T
APPLICANT: Lister-James, John
TITLE OF INVENTION: Technetium-99m Labeled Peptides for
TITLE OF INVENTION: Thrombus Imaging
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/335,832
FILING DATE: 05-JAN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5925331nan, Kevin E
REGIERARITON NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 92,216-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 53
CORRESSPONDERCE ADDRESS:
ADDRESSEBE: Banner & Allegretti, Ltd.
STREET: 10 South Wacker Drive Suite 3000
CITY: Chicago
STATE: 11linois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                    PRIOR APPLICATION 530

PRIOR APPLICATION DATA

APPLICATION NUMBER: US 08/212,186

FILING DATE: 11 MAR-1994

ATTONNEY AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815

REFERENCE/DOCKET NUMBER: P-LA 2041

TELECOMMUNICATION INFORMATION:
TELEFRAE: (619) 535-9001

TELEFRAE: (619) 535-909

INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTER.STICS:
LENGTH: 5 amino acids

TYPE: amino acids
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELEPHONE: 312-715-1000
TELERAX: 312-715-1234
TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
03-APR-1996
V: 530
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Best Local Similarity
Matches 5; Conserve
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Best Local Similarity
Matches 5; Conserv
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                                         GENERAL INFORMATION:
APPLICANT: Ruoslahti, Erkki
APPLICANT: Ruoslahti, Erkki
APPLICANT: Ruoslahti, Erkki
TITLE OF INVENTION: No. 5627263el Integrin-Binding Peptides
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 35; DB 1; Length 5; 100.0%; Pred. No. 3e+05;
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Patent No. 5912234

GENERAL INFORMATION:
APPLICANT: Ruosalatti, Erkki I.
APPLICANT: Rolvunen, Brkki
ITLE OF INVENTION: NOVEL INTEGRIN-BINDING PEPTIDES
NUMBER OF SEQUENCES: 27
CORRESCONDENCE ADDRESS:
ADDRESSE: CAMPBELL & FLORES, LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/425,238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER REALBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/625,695A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 21.7

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/158,001
FILING DATE: 24-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
FELECHOMINICATION INFORMATION:
TELECHONE: (619) 535-901
TELEPHONE: (619) 535-901
TELEPHONE: (619) 535-8949
INFORMATION FOR SEC ID NO: 8:
SEQUENCE CHARACTERISTICS:
Sequence 8, Application US/08425238
Patent No. 5627263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5; Conservative
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STRANDEDNESS: single
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                   CITY: San Diego
STATE: California
COUNTRY: USA
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Matches 5, Conserv
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US-08-625-695A-10
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Sequence 35, Appl
Sequence 24, Appl
Sequence 24, Appl
Sequence 1, Appli
Sequence 3, Aspli
Patent No. 5384309
Sequence 3, Appli
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| Sequence 10, Application US/08212186A
| Fatent No. 5536B14
| GENERAL INFORMATION:
| APPLICANT: Koivunen, Erkki I.
| ADDRESSEE: Campbell and Flores
| STATE: An Diego | STATE: California | COUNTRY: USA | COMPUTER: California |
| COUNTRY: USA | COMPUTER: Elpopy disk |
| COMPUTER: Elpopy disk | COMPUTER: Elpopy disk |
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| COMPUTER: Elpopy disk |
| COMPUTER: IBM PC compatible |
| COMPUTER: THE PERSENCE/DOCKET | US/08/212, 186A |
| CLASSIFICATION NUMBER: US/08/212, 186A |
| CLASSIFICATION NUMBER: 31, 815 |
| REPERSENCE/DOCKET NUMBER: BLANGEL |
| CELEPHONE: Glay 515-9901 |
| TELEPHONE: Glay 515-9901 |
| TELEPHONE: Elpopy disk |
| TELEPHONE: Elpopy |
| TELEPHONE: Elpopy disk |
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US-08-475-041-1
US-08-484-773-1
US-08-361-864-35
US-08-361-864-35
US-09-540-448-24
US-09-540-448-24
US-09-529-847-24
US-08-929-847-24
PCT-US93-09916-1
PCT-US93-09916-1
PCT-US93-09916-1
PCT-US94-01678-1
5384309-1
5384309-5
5384309-5
5384309-6
5384309-6
5384309-7
US-09-163-095-3
     Conservative
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Best Local Similarity
Matches 5; Conserv
CRGDC
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RESULT 2
US-08-425-238-8
Sequence 10, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 37, Appl
Sequence 37, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 4, Appl
Sequence 4, Appl
Sequence 11, Appl
Sequence 12, Appl
Sequence 14, Appl
Sequence 14, Appl
Sequence 16, Appl
Sequence 17, Appli
                                                                                                                                           September 22, 2004, 07:06:24; Search time 17 Seconds (without alignments) 15.184 Million cell updates/sec
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2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
  GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-425-238-8

US-08-425-695A-10

US-08-335-832-42

US-08-753-781-35

US-08-286-861-37

US-09-24-002-10

US-08-924-002-10

US-08-924-002-10

US-08-924-002-10

US-08-924-002-10

US-08-141-127-15

US-08-133-832-41

US-08-141-127-14

US-08-141-127-14

US-09-141-127-14

US-09-925-115-4

US-08-958-993A-1

US-08-958-993A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                389414 segs, 51625971 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                           OM protein - protein search, using sw model
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Match Length
                                                                                                                                                                                                                                                                                                       CRGDC 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Molmed Spa

TITLE OF INVENTION: MODIFIED CYTOKINES FOR USE IN CANCER THERAPY
FILE REFERENCE: P014717USM CLM
CURRENT APPLICATION NUMBER: US.10/287,811A
CURRENT PILING DATE: 2002-11-05
PRIOR APPLICATION NUMBER: IT MIZ000A000249
PRIOR APPLICATION NUMBER: IT MIZ000A000249
PRIOR FILING DATE: 2000-02-15
PRIOR APPLICATION UNMBER: C.I.P from US 10/218,906
PRIOR FILING DATE: 2001-02-13
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin Version 3.0
SEQ ID NO 12
LENGTH: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY: UNSURE
LOCATION: (1)..(5)
COTHER INCRMATION: where peptide is cyclic or linear
US-10-287-811A-12
                                    Sequence 3, Application US/10853895
GENERAL INFORMATION:
APPLICANT: Porizoni, Mirco
APPLICANT: Corti, Angelo
APPLICANT: Allen, Theresa
ITILE OF INVENTION: TUMOR TARGETED BRUG DELIVERY
ITILE OF INVENTION: SYSTEMS AND USES THEREOF
FILE REFERENCE: 11464-006-999 (108463-999004)
CURRENT FILING DATE: 2004-05-26
CURRENT FILING DATE: 2003-05-29
NUMBER OF SEQ ID NOS: 7
SEQ TEACH OF SEQ ID NOS: 7
SEQ TEACH OF SEQ ID NOS: 7
LENGTH: 5
LENGTH: 5
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US-10-287-811A-12
; Sequence 12, Application US/10287811A
; GENERAL INFORMATION:
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60.0%;
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Best Local Similarity 60.0
Matches 3; Conservative
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Best Local Similarity 60.0
Matches 3; Conservative
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                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
CAGANISM: Homo sapiens
US-10-853-895-3
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ORGANISM: Artificial
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RESULT 14
US-10-853-895-3
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Search completed: September 22, 2004, 07:19:49 Job time : 64 secs

1 CNGRC 5

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TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 60.0
Matches 3; Conservative
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Best Local Similarity 60.0
Matches 3; Conservative
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    Sequence 259, Application US/10714564A
GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
TITLE OF INVENTION: FUNCTIONS OF NONCLASSICAL CADHERINS
FILE REFRENCE: 100086.418
CURRENT APPLICATION NUMBER: US/10/714,564A
CURRENT FILING DATE: 2003-11-14
NUMBER OF SEQ ID NOS: 1402
SOTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 5;
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GENERAL INFORMATION:
APPLICANT: The Regents of the University of Colorado
APPLICANT: Koch, Tad
                                                                                                                                                                                                                                                                                       Score 25; DB 6; I
Pred. No. 6.5e+05;
                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                             ; OTHER INFORMATION: Exemplary cyclic peptide US-10-714-564A-259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Cyclic peptide US-10-785-924-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/10785924
GENERAL INFORMATION:
APPLICANT: Gilchrest, Barbara A.
                                                                                                                                                                                                                                                                                         71.4%;
80.0%;
                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 80.0
Matches 4; Conservative
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Best Local Similarity 60.0
Matches 3; Conservative
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US-10-714-564A-259
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PCT-US04-29095-2
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US-10-785-924-3
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Sequence 37, Application US/10839037

Sequence 37, Application US/10839037

Sequence 37, Application US/10839037

APPLICANT: NOSTENUIK, PAUL

APPLICANT: LIU, CHUAN-PA

PAPLICANT: LIU, CHUAN-PA

TITLE OF INVENTION: MELATED PROTEIN

TITLE OF INVENTION: RELATED PROTEIN

TITLE OF INVENTION: MUMBER: US/10/839,037

CURRENT APPLICATION NUMBER: US/09/843,221A

PRIOR APPLICATION NUMBER: 60/266,673

PRIOR APPLICATION NUMBER: 60/24,860

PRIOR FILING DATE: 2001-04-26

PRIOR FILING DATE: 2000-06-28

PRIOR FILING DATE: 2000-06-27

NUMBER OF SEQ ID NOS: 170

SOFTWARE: PATENTING DATE: 2000-06-27

NUMBER OF SEQ ID NOS: 170
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60.0%; Pred. No. 6.5e+05;
tive 0; Mismatches 2;
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60.0%; Pred. No. 6.5e+05;
iive 0; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial
FRATURE:
OTHER INFORMATION: tumor homing peptide
PCT-US04-29095-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: modified bovine PTH US-10-839-037-37
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Gaps
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GENERAL INFORMATION:
APPLICANT: Zhang, Dongxiao
TITLE OF INVENTION: METHODS OF SCREENING FOR MONOCLONAL
TITLE OF INVENTION: ANTIBODIES WITH DESIRABLE ACTIVITY
FILE REPERENCE: EPIT-07
CURRENT APPLICATION NUMBER: US/10/869,355
CURRENT FILING DATE: 2004-06-15
PRIOR APPLICATION NUMBER: 60/483,391
PRIOR FILING DATE: 2003-06-26
PRIOR FILING DATE: 2003-6-26
PRIOR FILING DATE: 2003-6-26
PRIOR FILING DATE: 2003-6-30
NUMBER OF SEQ ID NOS: 38
SOFTWARE FastSEQ for Windows Version 4.0
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                                                                                                                                                                                               APPLICANT: GRANDI Guido
APPLICANT: MASIGNANI Vega
APPLICANT: MASIGNANI Vega
APPLICANT: MASIGNANI Vega
APPLICANT: PIZZA MARIAGRAZIA
APPLICANT: RAPPUOLI Rino
APPLICANT: RAPPUOLI Rino
APPLICANT: RAPPUOLI Rino
APPLICANT: RAPPUOLI Rino
APPLICANT: SCARLATO Vincenzo
APPLICANT: SCARLATO Vincenzo
APPLICANT: SCARLATO Vincenzo
APPLICANT: SCARSELLI Maria
TITLE OF INVENTION: NEISERIALA ANTIGENIC PEPTIDES
FILE REFERENCE: 2300-1654 (PP01654.003)
CURRENT APPLICATION NUMBER: US-60/1611,983
CURRENT FILING DATE: 1999-10-29
NUMBER OF SEQ ID NOS: 37764
SOCTWARE: SeqWing9, version 1.02
SEQ ID NO 30763
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7 TYPE: PRT

ORGANISM: Oryctolagus cuniculus
US-10-869-355-8
                                                                                                                                                                 APPLICANT: CHIRON SpA
APPLICANT: GALEOTTI Cesira
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Best Local Similarity 100.
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ORGANISM: Neisseria
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2 RGDC 5
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Pred. No. 6.5e+05;
0; Mismatches 0; Indels
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; TITLE OF INVENTION: NEISSERIAL ANTIGENIC PEPTIDES
; FILE REFREENCE: 2300-1654 (PP01654.003)
; CURRENT APPLICATION NUMBER: US/10/111,983
; CURRENT FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: US-60/162616
; PRIOR FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 37764
; SOFTWARE: SEQWin99, Version 1.02
                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: NEISSERIAL ANTIGENIC PEPTIDES FILE REFERENCE: 2300-1654 (PP01654.003) CURRENT APPLICATION NUMBER: US/10/111,983 CURRENT FILING DATE: 2003-06-27 PRIOR APPLICATION NUMBER: US-60/162616 NUMBER OF SEQ ID NOS: 37764 SOFTWARE: SeqWin99, version 1.02 SEQ ID NO 4826
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Similarity 100.0%; Pred. No. 6.5e+05;
4; Conservative 0; Mismatches 0;
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100.0%; Pred. No. ...
0; Mismatches
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                                                                                                 ; Sequence 4826, Application US/10111983
; GENERAL INFORMATION:
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MORA Mariarosa
PIZZA Mariagrazia
RAPPUOLI Rino
RATTI Giulio
SCARLATO Vincenzo
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PIZZA Mariagrazia
RAPPUOLI Rino
RATTI Giulio
SCARLATO Vincenzo
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APPLICANT: GALEOTTI Cesira
APPLICANT: GRANDI Guido
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APPLICANT: GALEOTTI Cesira
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Best Local Similarity 100.
Matches 4; Conservative
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Best Local Similarity
Matches 4; Conserv
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; ORGANISM: Neisseria
US-10-111-983-18704
RGDC 4
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APPLICANT:
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APPLICANT:
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RESULT 10

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TITLE OF INVENTION: Method for Determining the Substrate Specificity of an Enzymatic TITLE OF INVENTION: Activity and a Device Therefor FILE REFERENCE: 2918-0102 CURRENT APPLICATION NUMBER: US/10/475,104 CURRENT PILING DATE: 2003-10-17 PRIOR APPLICATION NUMBER: PCT/EP02/04265 PRIOR FILING DATE: 2002-04-17 NUMBER OF SEQ ID NOS: 144 SOFTWARE: Patentin version 3.2 SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , OTHER INFORMATION: Description of Artificial Sequence: Synthetic RGDC sequence US-10-734-730-4
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100.0%; Pred. No. 6.5e+05;
iive 0; Mismatches 0;
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APPLICANT: Hellebust, Halldis
APPLICANT: Solbakken, Magne
TITLE OF INVENTION: Diagnostic/Therapeutic Agents
FILE REFERENCE: NIDN-10314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE KEFEKENES: NATURALISTS
CURRENT FILING DATE: 2003-12-15
PRIOR APPLICATION NUMBER: US/10/734,730
CURRENT FILING DATE: 2003-12-15
PRIOR FILING DATE: 2010-08-10
PRIOR FILING DATE: 1997-10-28
PRIOR FILING DATE: 1997-06-07
PRIOR APPLICATION NUMBER: 60/049,263
PRIOR FILING DATE: 1997-06-07
PRIOR APPLICATION NUMBER: 60/049,264
PRIOR FILING DATE: 1997-06-06
PRIOR FILING DATE: 1997-06-06
PRIOR FILING DATE: 1997-06-07
PRIOR FILING DATE: 1997-06-07
PRIOR FILING DATE: 1997-06-07
PRIOR FILING DATE: 1997-06-07
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                             ; FEATURE:
; OTHER INFORMATION: cell-adhesive peptide
US-10-475-104-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rongved, Pal
Hogset, Anders
Tolleshaug, Helge
Cuthbertson, Alan
Godal, Aslak
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Best Local Similarity 100.0
Matches 4; Conservative
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Gogstad, Geir
Bryn, Klaus
                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Conservative
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Best Local Similarity
Matches 4; Conserv
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ORGANISM: Unknown
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APPLICANT: DORRELL, Michael. I.
TITLE OF INVENTION: SELECTIVE R-CADHERIN ANTAGONISTS AND
TITLE OF INVENTION: METHODS
FILE REFERENCE: TSRI-987.1
CURRENT APPLICATION NUMBER: US/10/836,289
CURRENT PAPLICATION NUMBER: 60/467,188
FRIOR APPLICATION NUMBER: 60/467,188
FRIOR APPLICATION DATE: 2003-05-01
NUMBER OF SEQ ID NOS: 20
SOFTWARE: FASCEEQ for Windows Version 4.0
SEQ ID NO 13
                                                                                                                                                                                                                                                                                                                                                                                               Score 29, DB 1; Length 5;
Pred. No. 6.5e+05;
0; Mismatches 1; Indels
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FILE REFERENCE: TSRI-987.1PC;
CURRENT APPLICATION NUMBER: PCT/USO4/13212;
CURRENT APPLICATION NUMBER: PCT/USO4/13212;
CURRENT FILING DATE: 2004-05-05;
PRIOR APPLICATION NUMBER: 60/467,188;
PRIOR FILING DATE: 2003-05-01;
NUMBER OF SEQ ID NOS: 20
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13
LENGTH: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 13, Application US/10836289
GENERAL INFORMATION:
APPLICANT: THE SCRIPPS RESEARCH INSTITUTE
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ORGANISM: Artificial Sequence
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80.0%;
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ORGANISM: Artificial Sequence
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Hummel, Gerd
Jobron, Laurence
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Best Local Similarity 80.v
A: Conservative
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Panse, Soren
Scharn, Dirk
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Best Local Similarity
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US-10-475-104-1
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Sequence 77, Appl Sequence 13, Appl Sequence 13, Appl Sequence 14, Appli Sequence 4, Appli Sequence 4, Appli Sequence 18704, Appli Sequence 259, Appli Sequence 37, Appli Sequence 37, Appli Sequence 24, Appl Sequence 22, Appl Sequence 24, Appl Sequence 22, Appl Sequence 24, Appl Sequence 22, Appl Sequence 24, Appl Sequence 21, Appl Sequence 21, Appl Sequence 21, Appl Sequence 41, Appl Seq
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Appli
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Sequence 3
Sequence 3
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(5972 6/ptodata/1/paa/USOE NEW COMB.pep:*

(5972 6/ptodata/1/paa/USOT NEW COMB.pep:*

(5972 6/ptodata/1/paa/USOB NEW COMB.pep:*

(5972 6/ptodata/1/paa/USOB NEW COMB.pep:*

(5972 6/ptodata/1/paa/USOB NEW COMB.pep:*

(5972 6/ptodata/1/paa/USOB NEW COMB.pep:*)
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-665-668A-3
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Maximum Match 100%
Listing first 45 summaries
                                                                                         OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Match Length
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Perfect score:
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Sequence 3, Appli Sequence 17, Appl Sequence 303, Appl Sequence 353, Appl Sequence 37465, A Sequence 27465, A Sequence 281, Appl Sequence 281, Appl Sequence 209, Appl Sequence 6, Appli Sequence 1, Appli Sequence 4, Appli Sequence 4, Appli Sequence 1, Appli	ANGIOGENIC DISORDERS	gth 5; Indels 0; Gaps 0; AND
5 6 US-10-870-765-3 4 6 US-10-839-434-1 5 6 US-10-714-564A-303 5 6 US-10-714-564A-303 5 6 US-10-714-564A-1017 5 6 US-10-714-564A-1017 5 6 US-10-111-983-27465 5 6 US-10-719-564A-201 5 6 US-10-759-507-209 5 7 US-10-759-507-209 7 1 PCT-USO4-07269-5 7 1 PCT-USO4-07269-5 7 1 PCT-USO4-07269-6 7 1 PCT-USO4-07269-6 7 1 PCT-USO4-16828-1 7 1 US-09-446-274B-4 7 1 US-09-446-274B-4	ALIGNMENTS  ion US/10342081  e, Milind D. Scott John A.  Thomas D.  "Stuart J.  "Ashlad R.  PHARWACEUTICALS FOR THE IMAGING OF 2003-01-14 NUMBER: US/10/342,081 2003-01-14 NUMBER: US 09/599,295 000-06-21 : 169 ersion 3.2  I Sequence Synthetic Construct URE Cyclic amino acid	30; DB 6; Len No. 6.5e+05; matches 1; TUTE RIN ANTAGONISTS
22 28 29 30 31 31 31 32 33 33 34 35 36 36 37 38 38 39 39 30 30 30 30 30 30 30 30 30 30	ULT 1  0-342-081-77  quence 77, Applicat WERAL INFORMATION: PPLICANT: Rajopadhy PPLICANT: Rajopadhy PPLICANT: Barrett, PPLICANT: Barrett, PPLICANT: Harris, PPLICANT: Harris, PPLICANT: Harris, PPLICANT: Garpente PPLICANT: Applicat URLENT: FILLUS DATE: 2 URRENT FILLUS DATE: 2 URRENT FILLUS DATE: 2 URRENT PILLUS DATE: 2 URRENT FILLUS DATE: 2 URNER OF SEQ ID NOS OFTWARE: PALCATION NO UNDER OF SEQ ID NOS OFTWARE: PATENTE: PATENTE: PATURE: PATURE	y Match Local Similarity hes 4; Consen 1 CRGDC 5 1 CRDC 5 2 04-13212-13 ence 13; Applicat RAL INFORMATION: LICANT: TRIEDLAN LICANT: PRIEDLAN LICANT: LICANT: LICANTION:
	US-1US-1US-1US-1US-1US-1US-1US-1US-1US-1	Quer Best Matc Oy Oy Db Db CT-US ; GENER ; APP ; APP ; TIT

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RESULT 15
US-10-081-258-11
Sequence 11, Application US/10081258
GENERAL INFORMATION:
APPLICANT: Liu, Shuang
TITLE OF INTENTION: ASCOrbic Acid Analogs For Metalloradiopharmceuticals
TITLE OF INTENTION: ASCORbic Acid Analogs For Metalloradiopharmceuticals
CURRENT FILING DAFE: 2002-02-22
CURRENT FILING DAFE: 2002-02-22
FRIOR FILING DAFE: 2001-02-26
NUMBER: OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 3.2
SEQ ID NO 11
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Pred. No. 5.5e+06;
0; Mismatches 1; Indels
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Best Local Similarity 80.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 1; Indels
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ORGANISM: Artificial Sequence
FRATURE:
OTHER INFORMATION: Synthetic construct
US-10-081-258-11
; SEQ ID NO 11

1. LENGTH: 5

TYPE: PRT

ORGANISM: Artificial Sequence

FRATURE:

OTHER INFORMATION: Synthetic Construct
US-10-033-769-11
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Best Local Similarity 80.0%;
Matches 4; Conservative
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Search completed: September 22, 2004, 07:18:39 Job time : 403 secs

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APPLICANT: Wickham, Thomas J
APPLICANT: Kovesdi, Imre
APPLICANT: Roelvink, Petrus W
APPLICANT: Realvink, Petrus W
APPLICANT: Brough, Douglas E
APPLICANT: Lizonova, Alena
TITLE OF INVENTION: ALTERNATIVELY TARGETED ADENOVIRUS
FILE REFERENCE: 205046
CURRENT APPLICATION NUMBER: US/60/208,451
CURRENT PILING DATE: 2000-05-31
NUMBER OF SEQ ID NOS: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 35; DB 33; 100.0%; Pred. No. 5.5e+06;
        Sequence 2, Application US/60208451 GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 5; Conservative
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; ORGANISM: Homo sapiens
US-60-208-451-2
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SOFTWARE: POSEQ ID NO 2
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APPLICANT: ROLVINK, PETRUS W
APPLICANT: BIOGLYINK, PETRUS W
APPLICANT: BINELD, DAVID
APPLICANT: BROUGH, DOUGLAS E
APPLICANT: LIZONOVA, ALENA
TITLE OF INVENTION: METHOD AND COMPOSITION FOR TARGETING AN ADENOVIRAL VECTOR
FILE REFERENCE: 220148
                                     APPLICANT: UNGER, EVAN C.
APPLICANT: WASTSUNAGA, TERRY ONICHI
APPLICANT: MATSUNAGA, TERRY ONICHI
APPLICANT: RAMASWAMI, VARADARAJAN
APPLICANT: ROMANOWSKI, MAREK J.
ITILE OF INVENTION: NOVEL TARGETED DELIVERY SYSTEMS FOR BIOACTIVE AGENTS
ITILE DEPERENCE: 5030-0001.24
CURRENT APPLICATION NUMBER: US/09/912,609
CURRENT FILING DATE: 2001-07-25
PRIOR FILING DATE: 2000-10-31
PRIOR PRILING DATE: 2000-10-31
PRIOR PRILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 131
SOFTWARE: PALENTIN VEY: 2.1
SEQ ID NO 9
LENGTH: 5
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OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-912-609-9
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100.0%; Pred. No. 5.5e+06;
ative 0; Mismatches 0;
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CURRENT FILING DATE: 2002-11-25
PRIOR APPLICATION NUMBER: PCT/US01/17391
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2000-09
PRIOR APPLICATION NUMBER: US 09/631,191
PRIOR APPLICATION NUMBER: US 60/208451
PRIOR APPLICATION NUMBER: US 60/208451
NUMBER: OF SEQ ID NOS: 31
SEQ ID NO 2
Sequence 9, Application US/09912609
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.0
Matches 5; Conservative
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Best Local Similarity 100.
Matches 5; Conservative
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ORGANISM: Homo sapiens
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Indels

0; Mismatches

Length 5;

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GENERAL INFORMATION:
GENERAL INFORMATION:
TOTLE OF INVENTION:
TITLE OF INVENTION: SIMULANEOUS IMAGING OF CARDIAC PERFUSION AND A VITRONECTIN
TITLE OF INVENTION: SIMULANEOUS IMAGING AGENT
FILE REFERENCE: BMS-2201
CURRENT APPLICATION NUMBER: US/09/995,388
CURRENT APLICATION NUMBER: US 60/253,324
PRIOR APPLICATION NUMBER: US 60/253,324
NUMBER OF SEQ ID NOS: 49
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
TYPE: PRI
TYPE: TYPE: PRI
TYPE: TY
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TITLE OF INVENTION: POLYPODAL CHELANTS FOR METALLOPHARMACEUTICALS
TILE REFERENCE: BMS-2204
CURRENT APPLICATION NUMBER: US/10/033,769
CURRENT FILING DATE: 2001-12-27
PRIOR PAPLICATION NUMBER: US 60/260,619
PRIOR FILING DATE: 2001-01-09
NUMBER OF SEQ 11
SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Synthetic Construct US-09-995-388-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-033-769-11; Sequence 11, Application US/10033769; GENERAL INFORMATION:
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RESULT 12 US-60-208-451-2

us-09-912-609-9.closed.rapm

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Length 5;
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SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 35; DB 20; 100.0%; Pred. No. 5.5e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 35; DB 20;
100.0%; Pred. No. 5.5e+06;
tive 0; Mismatches 0;
                                 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/627,035
FILING DATE: 27-Jul-2000
CLASSIFICATION NUMBER: US/09/627,035
PRIOR APPLICATION NUMBER: 08/212,186
APPLICATION NUMBER: 08/212,186
FILING DATE: CURROWN:
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REFERRNCE/DOCKET NUMBER: 31,815
REFERRNCE/DOCKET NUMBER: P-LA 9861
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-8499
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: S amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: both SEQUENCE DESCRIPTION: SEQ ID NO: 10: US-09-627-035-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Synthetic construct US-09-699-679A-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.
Best Local Similarity 100.
Matches 5; Conservative
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hes 5; Conservative
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US-09-912-609-9
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Matches
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GENERAL INFORMATION:
FROME SECONDARY STATES SERVER I.
FROME SECONDARY SERVER I.
FOR INVENTION: NOVEL INTEGRIN-BINDING PEPTIDES
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
FROME STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: Galifornia
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                      Sequence 37, Application US/09364597A
GENERAL INFORMATION:
APPLICANT: Ruoslahti, Erkki
APPLICANT: Rosolahti, Erkki
TITLE OF INVENTION: Novel Integrin-Binding Peptides
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4170 La Jolla Village Drive, Suite 700
STREET: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OMPUTER: TSW FC compatible
OMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 30-JUL-1999
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 35; DB 17; 100.0%; Pred. No. 5.5e+06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/158,001
FILING DATE: 24-00V-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,861
FILING DATE: 04-A0C-1994
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn
REGISTRATION NUMBER: 31,81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-LA 3419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: P-TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (858) 535-9001
TELEPAX: (858) 535-8949
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 5 amino acids
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US-09-364-597A-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
                                                                  US-09-364-597A-37
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US-09-627-035-10
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US-09-679A-24

US-09-679A-24

US-09-679A-24

Sequence 24, Application US/09699679A

SEMERAL INFORMATION:

APPLICANT: Unger, Evan C.

APPLICANT: Shen, Dekang

APPLICANT: Win, Guani;

TITLE OF INVENTION: Novel Targeted Compositions For Diagostics And Therapeutic Use

FILE REFERENCE: UNCRISOB

CURRENT PAPLICATION NUMBER: US/09/69,679A

FRIOR FILING DATE: 1994-12-22

PRIOR FILING DATE: 1996-06-06

PRIOR PELING DATE: 1996-06-06

PRIOR FILING DATE: 1996-06-06

PRIOR PELING DATE: 1996-06-01

PRIOR PELING DATE: 1996-06-01
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0; Gaps
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Markland Jr., Francis S.
APPLICANT: Bush Larry R.
APPLICANT: Swenson, Stephen
APPLICANT: Flores Sanchez, Eladio
TITLE OF INVENTION: THROMBOLYTIC AGENTS WITH ANTITHROMBOTIC
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                      Length 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: BM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/982,981
FLING DATE:
CLASSIPICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/753,781
FILING DATE: 02-DEC-1996
ATTORNEY AGENT INFORMATION:
NAME: McDaniels, Patricia A.
REGISTRATION NUMBER: 33.194
REFERENCE/DOCKET NUMBER: DIT 124.1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELERPHONE: 603.437.9077
                                                                                                                                                                                                                                                  100.0%; Score 35; DB 11; 100.0%; Pred. No. 5.5e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 35; DB 13;
100.0%; Pred. No. 5.5e+06;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 45, Application US/08982981
GENERAL INFORMATION:
                                                                                   45:
                 TELEPHONE: 312 913 0001
TELEFAX: 312 913 0002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Diatide, Inc. STREET: 9 Delta Drive
                                                                          INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                            Conservative
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Best Local Similarity 100.

Matches 5; Conservative
                                                                                                                                                            TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-753-781B-45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: peptide
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Best Local Similarity
Matches 5; Conserv
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GENERAL INFORMATION:
APPLICANT: Markland, Francis S
APPLICANT: Bush, Larry R
APPLICANT: Swenson, Stephen
APPLICANT: Sanchez, Eladio F
ITILE OF INVENTION: Thrombolytic Agents with Antithrombotic TITLE OF INVENTION: Properties
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
TITLE OF INVENTION: NOVEL INTEGRIN-BINDING PEPTIDES NUMBER OF SEQUENCES: 25
CORRESPONDENCES: 25
ADDRESSE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
STRET: San Diego
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CIDILITY: USA

CIP: 6606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

GURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/753,781B

FILING DATE: 02-DEC-1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Noonan, Kevin B

REGISTRATION NUMBER: 35,303

REFERENCE/POCKET NUMBER: 36,2056

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/625,695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3: McDonnell Boehnen Hulbert & Berghoff
300 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5.5e+06;
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FILING DATE:
CLASIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISCRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LA 9861
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 35; 100.0%; Pred. No.
                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (619) 535-900
TELEPAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5; Conservative
                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
OGY: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 300 South
CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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                                                                                                                                                                       ZIP: 92122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-753-781B-45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
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         Length 5;
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MEDIUM TYPE: Ploppy disk

MEDIUM TYPE: Ploppy disk

COMPUTER: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/575,461

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/961,889

FILING DATE: 04-JUN-1993

APPLICATION NUMBER: US 07/550,330

FILING DATE: 09-JUL-1990

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                           APPLICANT: Lob1, Thomas J.
APPLICANT: Chiang, Shiu-Lan
APPLICANT: Cardarelli, Pina M.
IITLE OF INVENTION: Cyclic Cell Adhesion Modulation
TITLE OF EQUENCES: 223
CORRESPONDENCE ADDRESS:
       100.0%; Score 35; DB 3; I
100.0%; Pred. No. 5.5e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 35; DB 9; I
100.0%; Pred. No. 5.5e+06;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tanabe #7126/PD1381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East, Fifth Floor
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 10, Application US/08625695
GENERAL INFORMATION:
APPLICANT: Ruoslahti, Erkki I.
APPLICANT: Roivunen, Erkki I.
                                                                                                                                                                                                                                         US-08-575-461-55; Sequence 55, Application US/08575461; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: BOSTICH, JUNE M.
REGISTRATION NUMBER: 31,238
REFRENCE/DOCKET NUMBER: Tanal
TELECOMMUNICATION INFORMATION:
TELEPAX: (619) 455-5100
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: Disulfide-bond
       Query Match 100.
Best Local Similarity 100.
Matches 5; Conservative
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Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: peptide
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GY: linear
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US-08-575-461-55
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                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 35; DB 1; Length 5; 100.0%; Pred. No. 5.5e+06; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 55, Application US/07961889
GENERAL INFORMATION:
APPLICANT: Lobb, Thomas J.
APPLICANT: Chiang, Shiu-Lan
APPLICANT: Chiang, Shiu-Lan
APPLICANT: Cardarelli, Pina M.
TITLE OF INVENTION: Cyclic Cell Adhesion Modulation
TITLE OF SEQUENCES: 223
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:

COMPUTER READABLE FORM:
MEDITUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: Elb FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/961,889
FILING DATE: 04-UN-1993
CLASSIFICATION 1514
PRIOR APPLICATION NUMBER: US 07/550,330
FILING DATE: 09-ULL-1990
ATTOMEY/AGENT INPORMATION:
MAND: ADDATE: OP-ULL-1990
ATTOMEY/AGENT INPORMATION:
MAND: ADDATE: OP-ULL-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Spensley Horn Jubas & Lubitz
1880 Century Park East, Fifth Floor
APPLICATION DATA:
APPLICATION NUMBER: US 08/158,001
FILING DATE: 24-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: HOOK, Gregory
REGISTRATION NUMBER: 38,701
REFERENCE/DOCKET NUMBER: FP-LA 1220
TELECOMMUNICATION INFORMATION:
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 37:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: BOSTICH, JUNE M.
REGISTRATION NUMBER: 31,238
REFERENCE/DOCKET NUMBER: Tar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
TELEPAK: (619) 455-5100
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
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; LOCATION: 1..5
US-07-961-889-55
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Best Local Similarity luv...
Si Conservative
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LENGTH: 5 amino acids
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                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY: circular
PCT-US94-13542-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 5 amino a
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                               amino acid
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US-07-961-889-55
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1 CRGDC 5

Title: Perfect score: Sequence:

OM protein

Run on:

Scoring table:

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 5

Database

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Sequence 7, Appli
Sequence 12, Appl
Sequence 6, Appli
Sequence 10, Appl
Sequence 14, Appl
Sequence 14, Appl
Sequence 14, Appl
Sequence 4, Appli
Sequence 4, Appli
Sequence 4, Appli
                                                                                                                                                                                                                                                                      Sequence 23, App
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 10, Ag
Sequence 44, A
Sequence 44, A
Sequence 1, Ag
Sequence 11, Sequence 1125,
Sequence 1125,
                                                                                                                                                                    Sequence 2, Al
Sequence 2, Al
Sequence 48,
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Sequence 11, 1
Sequence 77, 1
                                                Sequence 10,
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Sequence 9,
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Sequence 1
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GENERAL INFORMATION:
APPLICANT: La Jolla Cancer Research Foundation
TITLE OF INVENTION:
NOVEL INTEGRATION PROPERTY
OCRESPONDENCE 46
CORRESPONDENCE ADDRESS:
ADDRESSES: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
                                                                                                                                                                                                                                                          3 US-07-821-011B-23
3 US-07-821-011B-23
3 US-07-821-011B-12
3 US-07-821-011B-16
5 US-08-197-012-10
5 US-08-197-012-10
1 US-08-197-012-11
US-08-197-012-14
1 US-08-198-1
1 US-08-981-14
1 US-08-981-14
1 US-09-051-2488-1
1 US-09-051-2888-1
1 US-09-091-5888-1
1 US-09-091-5888-1
1 US-09-091-5888-1
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MEDIUM TYPE: Floppy disk
GOMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: PCT/US94/13542
FILING DATE: PCT/US94
                                             US-08-625-695-10
US-08-73-781B-45
US-08-92-981-45
US-09-627-035-10
US-09-627-035-10
US-09-912-609-9
US-10-31-31-31
US-09-995-388-48
US-09-995-388-48
US-10-081-258-11
US-10-081-258-11
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US-07-962-955-1
US-07-962-956-1
US-07-962-956-1
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: California
RY: USA
 92122
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PCT-US94-13542-37
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   results predicted by chance to have a l to the score of the result being printed, of the total score distribution.
                                                                                                                   9 ; Search time 402 Seconds (without alignments) 12.140 Million cell updates/sec
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1: /cgn2_6/prodata/2/paa/PCTUS_COMB.pep:*
2: /cgn2_6/prodata/2/paa/USO6_COMB.pep:*
4: /cgn2_6/prodata/2/paa/USO6_COMB.pep:*
5: /cgn2_6/prodata/2/paa/USO8_COMB.pep:*
5: /cgn2_6/prodata/2/paa/USO8_COMB.pep:*
7: /cgn2_6/prodata/2/paa/USO8_COMB.pep:*
7: /cgn2_6/prodata/2/paa/USO8_COMB.pep:*
9: /cgn2_6/prodata/2/paa/USO8_COMB.pep:*
10: /cgn2_6/prodata/2/paa/USO8_COMB.pep:*
11: /cgn2_6/prodata/2/paa/USO8_COMB.pep:*
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14: /cgn2_6/prodata/2/paa/USO8_COMB.pep:*
15: /cgn2_6/prodata/2/paa/USO8_COMB.pep:*
16: /cgn2_6/prodata/2/paa/USO8_COMB.pep:*
16: /cgn2_6/prodata/2/paa/USO9_COMB.pep:*
17: /cgn2_6/prodata/2/paa/USO93_COMB.pep:*
18: /cgn2_6/prodata/2/paa/USO93_COMB.pep:*
19: /cgn2_6/prodata/2/paa/USO93_COMB.pep:*
10: /cgn2_6/prodata/2/paa/USO99_COMB.pep:*
                   5.1.6
Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                        Fotal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                         6019581 seqs, 976053577 residues
                   GenCore version (c) 1993 - 2004
                                                                                                                     September 22, 2004, 07:08:29
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Maximum Match 100%
Listing first 45 summaries
                                                                                   sw model
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Gapop 10.0 , Gapext 0.5
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derived by analysis of
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35
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Match Length
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Pred. No.

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Score

Result . 8 THIS PAGE BLANK (USPTO)

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Score 24; DB 10; Length 5;
Pred. No. 1.2e+06;
1; Mismatches 1; Indels
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FILING DATE: 31-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: HOG1e, Doreen M.
REGISTRATION NUMBER: 36,361
REFERENCE/DOCKET NUMBER: BU94-15A2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 781-861-6240
TELEFAX: 781-861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68.6%;
                                                                                                                                                                                                                                                                TELEFAX: 781-861-9540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 60.0
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-09-018-194-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |:| |
1 CKGAC 5
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US-09-018-194-3
; Sequence 3, Application US/09018194
; Publication No. US20030175231A1
; RUBERAL INFORMATION:
; APPLICANT Year, Mina
; APPLICANT Year, Mina
; TITLE OF INVENTION: METHODS OF INDUCING HAIR GROWTH AND
TITLE OF INVENTION: COLCRATION
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
                                                                                                                                                                                                                                             APPLICANT: Yar. Mina
APPLICANT: Yar. Mina
TITLE OF INVENTION: METHODS FOR DIAGNOSING AND TREATING
TITLE OF INVENTION: ALZHEIMER'S DISEASE
FILE REFERENCE: BU96-09A2
CURRENT APPLICATION NUMBER: US/09/866,898
CURRENT FILING DATE: 2001-05-29
PRIOR FILING DATE: 1998-09-29
PRIOR PILING DATE: 1998-09-29
PRIOR PILING DATE: 1996-03-29
PRIOR FILING DATE: 1996-03-29
PRIOR FILING DATE: 1996-03-29
NUMBER OF SEQ ID NOS: 5
SSEQ ID NOS: 6
SEQ ID NOS: 6
SEQ ID NOS: 6
SEQ ID NOS: 6
SEQ ID NOS: 7
SED ID NOS: 7
SED
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MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible COMPATER: PATEM: PC-DOS/MS-DOS SOFTWARE: PATEMIN Release #1.0, Version #1.30 CURRENT APPLICATION NUMBER: US/09/018,194 FILING APPLICATION SI4 PRIOR APPLICATION NUMBER: US 08/793,683 FILING DATE: 30-AUG-1995 RADE APPLICATION DATA: US 08/298,941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 68.6%; Score 24; DB 9; I
Best Local Similarity 60.0%; Pred. No. 1.2e+06;
Matches 3; Conservative 1; Mismatches 1;
                                                                                                               Sequence 3, Application US/09866898
Patent No. US20020001988A1
GENERAL INFORMATION:
APPLICANT: Gilchrest, Barbara A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:

COTHER INFORMATION: Cyclic peptide
US-09-866-898-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Lexington
STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |:| |
1 CKGAC 5
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                                                                        US-09-866-898-3
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TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: No. US20030054027Alel Sequence
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; Publication No. US20040175361A1
; GENERAL INFORMATION:
    APPLICANT: Blaschuk, Orest W.
    APPLICANT: Blaschuk, Orest W.
    APPLICANT: Michaud, Stephanie D.
    TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
    TITLE OF INVENTION: FUNCTIONS OF NONCLASSICAL CADHERINS
    FILE REPREMENCE: 100086.418
    CURRENT APPLICATION NUMBER: US/10/714,564A
    CURRENT FILING DATE: 2003-11-14
    NUMBER: OF SEQ ID NOS: 1402
    SOFTWARE: FastSEQ for Windows Version 4.0
    SEQ ID NO 259
    LENGTH: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
71.4%; Score 25; DB 16; Length 5;
Best Local Similarity 80.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                      TAPLICANT: UNGERT, Evan C.
TITLE OF INVENTION: Charged Lipids and Uses For The Same
FILE REPREBLICE: UNGRESS.
CURRENT APPLICATION NUMBER: US/10/046,801
CURRENT PILING DATE: 2002-05-13
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 1997-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74.3%; Score 26; DB 14; I 100.0%; Pred. No. 1.2e+06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Exemplary cyclic peptide US-10-714-564A-259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; LOCATION: (5); OTHER INFORMATION: X is penicillamine US-10-046-801-24
                                                                                                                                                                         Sequence 24, Application US/10046801; Publication No. US20030054027A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 37
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 24
LENGTH: 5
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NAME/KEY: UNSURE
LOCATION: (5)
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                     2 RGDC 5
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US-10-714-564A-259
                                                                                                                                                        US-10-046-801-24
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APPLICANT: Osterkamp, Frank
APPLICANT: Userkamp, Gerd
APPLICANT: Hummel, Gerd
APPLICANT: Jobron, Laurence
TITLE OF INVENTION: Method for Determining the Substrate Specificity of an Enzymatic
TITLE OF INVENTION: Activity and a Device Therefor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                                                 APPLICANT: Nycomed Imaging AS
TITLE OF INVENTION: Improvements in or relating to
TITLE OF INVENTION: Improvements in or relating to
TITLE OF INVENTION: agents
FILE REFERENCE: REF/Klaveness/054
CURRENT APPLICATION NUMBER: US/10/722,075
CURRENT FILLING DATE: 2093-11-26
PRIOR APPLICATION NUMBER: US/08/960,054A
PRIOR FILLING DATE: 1997-10-29
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
OTHER INFORMATION: Description of Artificial
OTHER INFORMATION: Sequence:RGDC-Mal-FEG3400-DSPE
US-10-722-075-1
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; OTHER INFERMATION: cell-adhesive peptide
US-10-478-104-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: 2918-0102
CURRENT APPLICATION NUMBER: US/10/475,104
CURRENT FILING DATE: 2003-10-17
PRIOR APPLICATION NUMBER: PCT/EP02/04265
BRIOR PILING DATE: 2002-04-17
NUMBER OF SEQ ID NOS: 144
SOFTWARE: PatentIn version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Schneider-Mergener, Jens APPLICANT: Schuckweski, Mike APPLICANT: Reimer, Ulf APPLICANT: Dong, Liying APPLICANT: Panse, Soren
                                                                                                                                                 Sequence 1, Application US/10722075; Publication No. US20040141922A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/10475104 Publication No. US20040171097A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 100.
Matches 4; Conservative
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Best Local Similarity
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ORGANISM: Unknown
                                                                                                                            US-10-722-075-1
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LENGTH: 4
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TYPE: PRT
ORGANISM: Artificial
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Batent No. US20020102217A1

GENERAL INFORMATION:

APPLICANT: Nycomed Imaging AS

TITLE OF INVENTION: Improvements in or relating to diagnostic/therapeutic
FILE REFERENCE: REF/Klavenes/206

CURRENT APPLICATION NUMBER: US/09/925,715

CURRENT PILING DATE: 2010-08-10

NUMBER OF SEQ ID NOS: 27

SOFTWARE: PatentIn Ver. 2.1
                            Gaps
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US-09-925-715-4
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                          1; Indels
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ss 0; Indels
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                                                                                                                                                                                              Sequence 1, Application US/09765614B
Sequence 1, US20020102215A1
GENERAL INFORMATION:
APPLICANT: NYCOMED IMAGING AS:
ITILE OF INVENTION: IMPROVEMENTS in or relating to
ITILE OF INVENTION: adaptstic/therapeutic
ITILE OF INVENTION: agents
FILE REFERENCE: REF/Klaveness/054
CURRENT APPLICATION NUMBER: US/09/765,614B
CURRENT FILING DATE: 2001-07-10
NUMBER OF SEQ ID NOS: 31
SOUTHWARE: Patentin Ver. 2.1
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Description of Artificial CHER INFORMATION: Sequence:RGDC-Mal-PEG3400-DSPE US-09-765-614B-1
      Pred. No. 1.2e+06;
0; Mismatches 1
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    80.08;
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ORGANISM: Artificial Sequence
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                      4; Conservative
Best Local Similarity
Matches 4; Conserv
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Best Local Similarity
Matches 4; Conserv
                                                              1 CRGDC 5
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US-09-765-614B-1
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US-09-991-588B-1
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OTHER INFORMATION: The three amino acid sequence RGD which occurs on Fibronectine ce
OTHER INFORMATION: 11 adhesion protein is modified with cystine to provide RGDC
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GENERAL INVORMITION:

APPLICANT: Schwarztz, Jeffrey,

APPLICANT: Danahy, Michael P

APPLICANT: Gawalt, Ellen S.

APPLICANT: Schwarzbauer, Jean E.

APPLICANT: Schwarzbauer, Jean E.

APPLICANT: Midwood, Kim S.

APPLICANT: Midwood, Kim S.

APPLICANT: AVAILTONI, Michael D.

TITLE OF INVENTION: ENHANCED BONDING LAYERS ON TITANIUM MATERIALS

FILE REPERENCE: 2025, 571-1 USA

CURRENT APPLICATION NUMBER: US 60/389, 574

PRIOR APPLICATION NUMBER: US 60/389, 574

PRIOR APPLICATION NUMBER: US 60/389, 574

PRIOR PILING DATE: 2001-06-22

PRIOR APPLICATION NUMBER: US 60/300, 144

PRIOR PILING DATE: 1997-00-22

PRIOR PILING DATE: 1997-00-22

PRIOR PILING DATE: 1997-00-24

PRIOR PILING DATE: 1997-01-13

PRIOR PILING DATE: 1997-01-13

PRIOR PILING DATE: 1997-01-13

PRIOR PILING DATE: 1996-10-17

NUMBER OF SEQ ID NOS: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
; OTHER INFORMATION: Purchased commercially or sequence is synthesized
US-09-991-588B-1
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Sequence 1, Application US/09991588B
Publication No. US20030219429A1
GENERAL INFORMATION:
APPLICANT: Budary, John A.
TITLE OF INVENTION: Compositionand Method for Bone Regeneration
FILE REFERENCE: 1008-120.US
CURRENT APPLICATION NUMBER: US/09/991,588B
CURRENT APPLICATION NUMBER: US/09/991,588B
PRIOR FILING DATE: 1998-07-24
NUMBER OF SEQ ID NOS: 23
SEQ ID NO 1
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                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 100.0
Matches 4; Conservative
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Sequence 48 Application US/09995388

Sequence 48 Application US/09995388

Publication No. US20020106325A1

GENERAL INFORMATION:
APPLICANT: CATPENTEN: JE., Alan P.
TITLE OF INVENTION: SIMULTANEOUS IMAGING OF CARDIAC PERFUSION AND A VITRONECTIN TITLE OF INVENTION: RECEPTOR TARGETED IMAGING AGENT FILE REFERENCE: BMS-2201
CURRENT APPLICATION NUMBER: US/09/995,388
CURRENT FILING DATE: 2001-11-27

PRIOR APPLICATION NUMBER: US 60/253,324

PRIOR FILING DATE: 2000-11-27
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TITLE OF INVENTION: POLYPODAL CHELANTS FOR METALLOPHARMACEUTICALS
TITLE OF INVENTION: 2014 POLYPODAL CHELANTS FOR METALLOPHARMACEUTICALS
FILE REFERENCE: BMS-2014 POLYPODAL CURRENT FILING DATE: 2001-12-27
PRIOR PILING DATE: 2001-12-27
PRIOR PILING DATE: 2001-10-9
NUMBER OF SEQ ID NOS: 11
SEQ ID NO 11
LENGTH: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 5;
                                                                                                                                                                                         100.0%; Score 35; DB 14; 100.0%; Pred. No. 1.2e+06;
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80.0%; Pred. No. 1.2e+06;
iive 0; Mismatches 1.
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, OTHER INFORMATION: Synthetic Construct
US-10-033-769-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 11, Application US/10033769
Publication No. US20020094316A1
GENERAL INFORMATION:
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SOFTWARE: PatentIn version 3.2
SEQ ID NO 48
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
  PRIOR FILING DATE: 2000-05-31
                    NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin Ver. 3.1
SEQ ID NO 2
LENGTH: 5
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Best Local Similarity 100.
Matches 5; Conservative
                                                                                                      TYPE: PRT; ORGANISM: Homo sapiens
US-10-304-160-2
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US-09-995-388-48
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US-10-033-769-11
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APPLICANT: RAMASWAMI, VARADRAJAN
APPLICANT: RAMASWAMI, VARADRAJAN
APPLICANT: RAMANOWSKI, MAREK J.
TITLE OF INVENTION: NOVEL TRREFEED DELIVERY SYSTEMS FOR BIOACTIVE AGENTS
FILE REFERENCE: 5030-0001.24
CURRENT FILING DATE: 2001-07-25
FRIOR APPLICATION NUMBER: 09/703,474
PRIOR FILING DATE: 2000-10-31
PRIOR PILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 131
SOFTWARE: PATENTIN UNIVERS: 09/478,124
NUMBER OF SEQ ID NOS: 131
SEQ ID NO 9
LENGTH:
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APPLICANT: ROLLVINK, PETRUS W
APPLICANT: RIFELD, DAVID
APPLICANT: BITNELD, DAVID
APPLICANT: BROUGH, DOUGLAS E
APPLICANT: LIZONOVA, ALENA
TITLE OF INVENTION: METHOD AND COMPOSITION FOR TARGETING AN ADENOVIRAL VECTOR
FILE REPRENCE: 2201448
CURRENT APPLICATION NUMBER: US/10/304,160
CURRENT PILING DATE: 2002-11-25
PRIOR APPLICATION NUMBER: PCT/US01/17391
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2000-08-09
PRIOR FILING DATE: 2000-08-09
PRIOR FILING DATE: 2000-08-09
PRIOR FILING DATE: 2000-08-09
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OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-912-609-9
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100.0%; Pred. No. 1.2e+06;
ative 0; Mismatches 0;
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100.0%; Pred. No. 1.2e+06;
Ative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
                                                                                                                          Query Match
Best Local Similarity 100.
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                                                                                  TOPOLOGY: circular
US-09-364-597A-37
                                                                amino acid
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Best Local Similarity
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Gaps

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US-09-364-597A-37
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Sequence 9, Appli
Sequence 2, Appli
Sequence 48, Appl
Sequence 11, Appl-
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Sequence 1, Appli
Sequence 24, Appl
Sequence 259, Appl
Sequence 3, Appli
Sequence 3, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Appl
Sequence 4, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                             (without alignments)
12.949 Million cell updates/sec
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Sequence 1,
                                                                                                                                                     September 22, 2004, 07:10:50 ; Search time 124 Seconds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | Cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
| Cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*
| Cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
| Cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*
| Cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*
| Cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*
| Cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
| Cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
| Cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
| Cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
| Cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
| Cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*
| Cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*
| Cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*
| Cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-304-160-2

US-10-304-160-2

US-10-309-53-88-48

US-09-925-715-4

US-09-912-715-4

US-09-912-715-4

US-10-179-743A-1

US-10-179-743A-1

US-10-046-801-24

US-10-046-801-24

US-10-10-14-564A-259

US-09-018-194-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1342398 segs, 321133274 residues
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                       OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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35
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Match Length
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                                                                                                                                                                                                                                                                   Title:
Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Minimum DB Maximum DB
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PDD 13 A ADD 14 A ADD 15 A ADD 17 A A A A A A A A A A A A A A A A A A	107 107 8,
9-765-086-8 9-840-277-37 10-603-2217-107 10-603-218-107 10-632-348-24 10-652-244-24 10-652-244-24 10-006-869-233 10-006-869-334 10-006-869-334 10-006-869-334 10-006-869-334 10-26-369-334 10-264-374-8 10-26-36-38 10-26-36-38 10-26-36-38 10-26-36-38 10-26-36-38 10-26-36-38 10-26-36-38 10-26-36-38 10-26-36-38 10-26-36-38 10-26-36-38 10-26-36-38 10-26-36-38 10-27-39-30-38 10-395-032-338	US-10-666-696-1075 US-10-653-048-1075 US-10-264-374-8
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1 1 1 1 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	4 4 4 6 4 0

## ALIGNMENTS

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S-09-546-597A-37

S-09-546-597A-37

S-09-546-597A-37

S-09-546-597A-37

Sequence 37, Application US/09364597A

Patent No. US20020103130A1

GENERAL INFORMATION:
APPLICANT: Roisbant, Erkit
APPLICANT: Campubli & Flores Lip
STREET: 4370 La Jolia Village Drive, Suite 700

CITY: San Diego
STARE: Campbell & Flores Lip
STREET: 4370 La Jolia Village Drive, Suite 700

STARE: California
COUNTRY: USA

ZIP: 937122

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Bap PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: BatentIn Release #1.0, Version #1.25

CURRENT PAPLICATION DATA:
APPLICATION NUMBER: US/09/364,597A

FILING DATE: 30-UUL-1999

CLASSIFICATION NUMBER: US/09/364,597A

FILING DATE: 24-NOV-1993

PRIOR APPLICATION NUMBER: US/09/364,597A

FILING DATE: 04-AUC-1994

ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: P-LA 3419

FELENCOMMUTER: P-LA 3419

TELESCOMMUTER: P-LA 3419

TELESCOMMUTER: ROS 535-8949
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CC The invention relates to a composition comprising a bioactive agent homogeneously dispersed in a targeted matrix (polymer and targeting consisted in a targeted matrix for use as a delivery consisted included are a targeted matrix for use as a delivery vehicle comprising a polymer associated with a targeting ligand, consonated the bioavailability of an agent comprising administration of the composition and treating cancer comprising administration of the composition. The method is useful for targeted delivery of a drug, especially in cancer therapy. The targeting ligand may be a peptide. Examples of targeting peptides are disclosed including cathepsin-D combatrate peptides, peptides targeting receptors in the brain and kidney, peptides targeting the RGD (Arg-Gly-Asp)-motif in, e.g., antibodies, competides targeting the angiogenic endothelium of solid tumours, tissue specific peptides (e.g. of lung, skin, pancreas, intestine, uterus, adrend adrend and retina), and cathonic cancer-targeting peptides. The present sequence is a peptide targeting ligand disclosed in the invention xx

Query Match
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CRGDC 5 ||||| 1 CRGDC 5

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Search completed: September 22, 2004, 07:50:29 Job time: 122 secs

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                                                                                                                                                                             Composition comprises technetium-99m and polyamide reagent which binds to thrombi, useful as scintigraphic imaging agent for imaging sites of thrombus formation in vivo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; adenoviral coat protein; non-native ligand; cell-surface receptor;
therapy; anti-tumour agent; tumour necrosis factor; cancer; brain; lung;
ovary; breast; prostate.
                                                                                                                                                                                                                                                          The present sequence is that of a peptide that acts as a ligand for the dPIIb/IIIa receptor. The invention relates to radiolabeled reagents that are scintigraphic imaging agents for imaging sites of thrombus formation in vivo. The reagents each comprise a specific binding compound, such as the present peptide, that is capable of binding to at least 1 component of a thrombus, and which is covalently linked to a radiolabel-binding moiety. A method for using such a reagent labeled with technetium-99m to image a thrombus site in a mammalian body is claimed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Adenoviral coat protein which permits production of adenoviral vectors that bind and infect host cells not naturally infected by adenovirus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 35; DB 3; Length 5; 100.0%; Pred. No. 1.4e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human ligand #2 attached to an adenoviral vector.
                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                    Example 2; Col 15-16; 27pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAE17982 standard; peptide; 5 AA.
              98US-00141127
                                        92US-00886752
                                                    93WO-US004794.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-MAY-2001; 2001WO-US017391.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-MAY-2000; 2000US-0208451P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-MAY-2002 (first entry)
                                                                                                                        Dean RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wickham TJ, Kovesdi I,
                                                                                                                                                  WPI; 2000-498061/44.
                                                                                             (DIAT-) DIATIDE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-147620/19
                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GENV-) GENVEC INC
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                                                                                                                        Lister-James J,
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                                                                                                                                                                                                                                                                                                                                                                                         Sequence 5 AA;
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              27-AUG-1998;
                                                    21-MAY-1993;
05-JAN-1995;
                                       21-MAY-1992;
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The invention relates to adenoviral coat proteins comprising various non-
contive ligands. The invention provides a method of controlled gene
coxpression utilising selectively replication competence and also a method
and a composition for targetting an adenoviral vector. A system
comprising a cell having a non-native cell-surface receptor, and a virus
comprising a non-native ligand which binds the non-native cell-surface
creceptor of the cell is useful for propagating a virus and also for
assaying gene function. The system is also useful for isolating a nucleic
acid encoding a product comprising a desired property. Further the system
is useful for identifying functionally related coding sequences.
Cateropeutic agent such as anti-tumour agent, preferably tumour necrosis
therapeutic agent such as anti-tumour agent, preferably tumour necrosis
catedor and a second non-native nucleic acid encoding an agent that
catedor and a second non-native nucleic acid encoding an agent that
catedor and a second non-native nucleic acid encoding an agent that
canimal. The therapeutic agent can be useful for treating an
canimal. The therapeutic agent can be useful for treat cancer of the brain,
continued ingand attached to an adenoviral vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Targeting ligand; bloactive agent; polymer matrix; cancer; cytostatic; cathepsin-D substrate; peptides; neuroreceptor; adrenal receptor; fibronectin; vitronectin; integrin; RGD motif; angiogenic endothelium; tumour; cationic cancer-targeting peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Targeted delivery system comprising a bioactive agent homogeneously dispersed in a targeted matrix is especially useful in cancer therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Finbronectin-binding integrin alphas-betal targeting peptide #11.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 35; DB 5; 100.0%; Pred. No. 1.4e+06; ive 0; Mismatches 0;
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comprises various non-native ligands.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABUS9650 standard; peptide; 5 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 42; Page 38; 46pp; English.
                                     Claim 4; Page 40; 45pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-JUL-2001; 2001US-00912609.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-JAN-2000; 2000US-00478124
31-OCT-2000; 2000US-00703474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (MATS/) MATSUNAGA T O.
(RAMA/) RAMASWAMI V.
(ROMA/) ROMANOWSKI M J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-208921/20.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 5 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABU59650;
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This sequence represents a peptide ligand for the fibrin polymerisation site. The invention relates to a complex (A) for thrombus imaging comprises technetium-99m (Tc-99m) completed with a reagent comprising a peptide (P) with 4 to 100 amino acids sequence and a Tc-99m binding moiety covalently bound to (P). (P) is selected from a linear peptide ligand for a GPIIb/IIIa receptor not comprising the amino acid sequence argantatele, a peptide ligand for a polymerisation site of fibrin, and a cyclic peptide ligand for the GPIIb/IIIa receptor. The thrombus imaging reagents provided by the present invention can be used for visualising thrombi in a mammalian body when Tc-99m is labelled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A complex used for thrombus imaging comprises technetium-99m complexed with a peptide ligand for GPIIb/IIIa receptor.
                                                                                                                                                                                                  Thrombus imaging, fibrin polymerisation site; technetium-99m; Tc-99m; GPIIb/IIIa receptor; cyclic peptide ligand.
                                                                                                                                                  Peptide ligand for fibrin polymerisation site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 2; Col 13-14; 18pp; English.
       AAY54976 standard; peptide; 5 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                     95US-00484773.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92US-00886052.
94US-00273274.
                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dean RT, Lister-James J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (DIAT-) DIATIDE INC.
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                                                                                                                                                                                               Thrombus imaging;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-MAY-1992;
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                                                                                                      15-FEB-2000
                                                                                                                                                                                                                                                                                                                       US5968476-A.
                                                                                                                                                                                                                                                                                                                                                                      19-OCT-1999
                                                                                                                                                                                                                                                                       Synthetic.
                                                         AAY54976;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to reagents (A) for preparing thrombus imaging agents comprising specific binding peptides (I) and a technetium-99m binding group (II) covalently attached to the specific binding peptide. (I) is a ligand for the GPIID/IIIa receptor and can be a cyclic or linear peptide not containing the Arg-Gly-Asp (RGD) sequence. (I) are specific for thrombi, and are small and therefore are rapidly cleared from blood and background tissue. (A) are used to produce scintigraphic imaging agents for detection of thrombi in vivo. The present sequence is one such TC-99m labelled peptide.
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                                                                                                                                                  Gaps
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                                                                                            100.0%; Score 35; DB 2; Length 5; 100.0%; Pred. No. 1.4e+06; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 35; DB 2; Length 5; 100.0%; Pred. No. 1.4e+06; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thrombus imaging agent; GPIIb/IIIa receptor; thrombus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Reagent for preparing thrombus imaging agent.
                                                                                                                                                                                                                                                                                                                                                       ADE25491 standard; peptide; 5 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91US-00807062.
92US-00886752.
94US-00264176.
94US-00273274.
95US-00480551.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tc-99m labelled peptide #19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-JAN-2004 (first entry)
inexpensively synthesised
                                                                                                                                             5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lister-James J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (DIAT-) DIATIDE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-253220/21.
                                                                                         Query Match
Best Local Similarity
Matches 5; Conserv
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Best Local Similarity
                                                                                                                                                                                        1 CRGDC 5
                                                                                                                                                                                                                                       CRGDC 5
                                               Sequence 5 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US5888474-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-NOV-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                      ADE25491;
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                                                                                                                                                                                                                                                                                                          ADE25491
ID ADE25491
XX ADE25
XX ADE25
XX DE 29-JA
XX Throm
XX Throm
XX Synth
XX ON-FE
PR 27-NO
PR 27-
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                             Gaps
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/ Match 100.0%; Score 35; DB 3; Length 5; Local Similarity 100.0%; Pred. No. 1.4e+06; les 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                           AAY95465 standard; peptide; 5 AA.
                                                                                                                                                                                                                       GPIIb/IIIa receptor ligand.
                                                                                                                                                                                             10-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                         04-JUL-2000
                                                                                                                                                                                                                                                                                        Synthetic
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1 CRGDC 5 CRGDC

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RESULT 15 AAYS4976

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The invention relates to new thrombolytic agents which comprise a thrombolytic proteinase covalently linked to a targetting compound capable of specifically binding to a component of a thrombus. The thrombolytic agents can be used for eliminating thrombi in vivo in, myocardial infarction, cerebral ischaemia, deep vein thrombosis or myocardial infarction, cerebral ischaemia, deep vein thrombosis or used to image thrombi for diagnostic purposes. The thrombolytic agent can also be used to image thrombi for diagnostic purposes. The thrombolytic agents are specifically targetted to thrombus sites in vivo and have minimal hamaourhagic side effects and side effects related to non-specific protecolysis. The present sequence represents a specifically claimed targetting peptide. (Updated on 25-MAR-2003 to correct PI field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Reagent useful for preparing thrombus imaging agent - comprises peptide covalently linked to technetium binding moiety which is technetium labelled and binds to thrombus component.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Technetium-99M label; thrombus imaging; GPIIb/IIIA receptor; ligand;
                                                                                                         New thrombolytic agents - comprise thrombolytic proteinase covalent
linked to targetting compound for binding to component of thrombus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GPIIb/IIIa receptor ligand, with technetium-99M binding moiety.
                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 35; DB 2; Length 5; 100.0%; Pred. No. 1.4e+06; ive 0; Mismatches 0; Indels
                                             Flores Sanchez E;
                                               Swenson S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW50594 standard; peptide; 5 AA.
(DIAT-) DIATIDE INC.
(UYSC-) UNIV SOUTHERN CALIFORNIA.
                                                                                                                                                      Claim 10; Page 65; 79pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91US-00653012.
91US-00807062.
92US-00886052.
94US-00264176.
95US-00480551.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dean RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                       5; Conservative
                                             Bush LR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1998-239148/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (DIAT-) DIATIDE INC.
                                                                            WPI; 1998-333336/29
                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        binding moiety
                                                                                                                                                                                                                                                                                                                                                                           Sequence 5 AA;
                                             Markland FS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-JUN-1995;
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22-JUN-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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The invention relates to peptides having specific binding specificity for fibronectin-binding and vitronectin-binding integrins, and in particular fibronectin-binding and vitronectin-binding integrin. The peptides can be used in a method of preventing integrin. The peptides can be used in a method of preventing integrin. The peptides can be used in a method of cells with a soluble peptide selected from the sequences shown in AAY21561, AAY21563 and AAY21586; or (b) contacting the cells with a soluble peptide comprising the sequence -NGR- selected from the sequences contacting the sequence shown in AAY21571. The peptides are useful for inhibiting metastatic process with which fibronectin adhesion is associated and also for inhibiting alpha v beta 1-mediated cell attachment to fibronectin, or inhibiting alpha v beta 1-mediated cell attachment to fibronectin, are also useful for promocting attachment to vitronectin. The peptides are also useful for promocting attachment to fibronectin. The peptides are also useful for promocting attachment to fibronectin.
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                               The invention relates to a reagent for preparing a thrombus imaging agent. It comprises: (a) a specific binding peptide (BP) having a sequence of 4-100 amino acids; and (b) a technetium-99m binding moiety (TBM) covalently linked to the peptide which binds to a component of a thrombus. TBM forms an electrically neutral complex with technetium-99m. The small size of the peptide component of the reagent enhances blood and background tissue clearance and it is easy to prepare. This sequence represents a GPIDA/IIIa receptor binding peptide covalently linked to a
                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Integrin; fibronectin; vitronectin; extracellular matrix protein; metastatic; fibronectin adhesion; alpha5betal integrin.
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                                                                                                                                                                                                                                                               Length 5;
                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                             100.0%; Score 35; DB 2; L
100.0%; Pred. No. 1.4e+06;
iive 0; Mismatches 0;
Example 2; Col 11-12; 18pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY21570 standard; peptide; 5 AA.
                                                                                                                                                                                    technetium-99m binding moiety
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94US-00212186.
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                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Integrin-binding peptide.
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Best Local Similarity
5; Conserve
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                                                                                                                                                                                                                                                                                                                                        1 CRGDC 5
                                                                                                                                                                                                                            Sequence 5 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11-MAR-1994;
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The present sequence represents a synthetic peptide which acts as an antagonist to integrin receptors. The invention provides various synthetic peptides which act as cell adhesion modulators because they mimic extra-cellular matrix ilgands or other cell adhesion ligands that bind to receptors such as integrin receptors, including fibronectin, laminin, LFA-1, MAC-1, p150,95, vitronectin and gpIIb/IITa receptors. Some of the peptides contain the amino acid sequence Arg-Gly-Asp (RGD) Others contain non-RGD sequences, for e.g RCD sequences, and reverse useful in modulating cell adhesion, including adhesion related to fibronectin, as well as leukocyte adhesion to endothelial cells. They are prevention of diseases which relate to cell adhesion, e.g. adult prevention of diseases which relate to cell adhesion, e.g. adult
                                                                                                                                                                                                                                                                                            New cyclic peptide(s) and peptidomimetic compounds - are integrin receptor antagonists useful in modulating cell adhesion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Targetting peptide #45 useful as component of thrombolytic agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thrombolytic agent; thrombolytic proteinase; blood clot; fibrin; thrombus; antithrombotic activity.
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Ouery Match

Doublest Local Similarity 100.0%; Pred. No. 1.4e+06;

Matches 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                            Chiang S;
                                                                                                                                                                                                                                                                                                                                                Example 9; Col 42; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW64952 standard; peptide; 5 AA.
                                                                                     95US-00485019.
                                                                                                                      90US-00550330.
                                                                                                                                      91WO-US004862
93US-00961889
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                                                                                                                                                                                       (TANA ) TANABE
                                                                                                                                                                                                                          Cardarelli PM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5 AA;
                                                                                   07-JUN-1995;
                                                                                                                                      09-JUL-1991;
                                                                                                                    09-JUL-1990;
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23-SEP-1998
                US5721210-A
                                                 24-FEB-1998
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                                                                                                                                                                                               Synthetic; fibronectin; vitronectin; integrin; binding motif; adhesion; extracellular matrix protein; tumour metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptides AAW03483-508 are examples of synthetic peptides generated to bind to the fibronectin/vitronectin-binding integrin alpha(5)beta(1). They are synthesised to contain the alpha(5)beta(1)-integrin peptide binding metifs: DGR, NGR or RGD. The peptides interfere with the binding of fibronectin and vitronectin to this integrin and thus may be used to block integrin-mediated cell adhesion to extracellular matrix proteins, esp. to inhibit tumour metastasis. (Updated on 25-MAR-2003 to correct PF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic integrin-binding peptide(s) - useful for inhibiting tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Integrin receptor antagonist, cell adhesion modulator, leukocyte, extracellular matrix, fibronectin, ARDS, thrombosis, inflammation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                          Alpha(5)-Beta(1) integrin binding peptide 10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Integrin receptor antagonist peptide 38.
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                                        AAW03492 standard; peptide; 5 AA.
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                                                                                                                                                                                                                                                                                                                                                         94US-00212186.
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                                                                                                                               (first entry)
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                                                                                                               (revised)
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                                                                                                                                                                                                                                                                                                                                                        11-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                                        27-SEP-1993;
                                                                                                         25-MAR-2003
24-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-AUG-1998
                                                                                                                                                                                                                                                                                    US5536814-A
                                                                                                                                                                                                                                                                                                                       16-JUL-1996
                                                                                                                                                                                                                                                   Synthetic.
                                                                        AAW03492;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ۲,
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       RESULT 9
AAW03492
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The invention relates to reagents for scintigraphic imaging of a thrombus in-vivo, comprising (A) a specific binding compound capable of binding to at least one component of a thrombus, covalently linked to (B) a technetium-99m-binding moiety. Specific peptides constituting the reagents are claimed as new. The present peptide is one such peptide. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Reagent for scintigraphic imaging of thrombi with 99m technetium - comprises synthetic peptide which binds to thrombus covalently coupled to metal binding gp., rapidly cleared from blood and tissue.
                                                                                                                                                                                                                                                                   The peptide sequence is an example of a highly generic sequence contg. the RGD motif. Compounds contg, these lipid peptides are useful as cell migration inhibitors in cell adhesion membranes or cell culture bodies. See also AAR29048-54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gp IIb/IIIa receptor ligand used in scintigraphic imaging of thrombi
                                                                                                   New synthetic peptide lipids or salts - useful as cell migration inhibitors, cell adhesion membranes and cell culture bodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Scintigraphy, thrombus, thrombi, imaging, specific binding, technetium-99m, radiolabelled, Gp IIb/IIIa receptor ligand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           h 100.0%; Score 35; DB 2; Length 5; Similarity 100.0%; Pred. No. 1.4e+06; 5; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                   Disclosure; Page 3; 9pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR69325 standard; peptide; 5 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 41; Page 46; 61pp; English
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Best Local Similarity
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25-JUN-1995
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The sequences given in AAR76185-200 and AAR79073-94 are high affinity integrin binding peptides which bind to various integrins. Peptides which bind to alphas/betal integrins contain the motifs given in AAR76185-86 and alphav/betal integrins are also contain the motif given in AAR76187. Alphav/betas integrins are also bound by RGD containing peptides. These peptides assume a conformationally stabilised configuration which is due to the formation of a disulphide bond, a peptide bond or a lactam bond. These peptides may be used for isolating the complementary integrin from a sample mixture by contacting them under ionic conditions to allow binding of the integrin to the peptide and then separating the integrin from the peptide. They can be used for attaching cells to a substrate, by binding when to the substrate with the cell. The peptides promote wound healing when applied locally and inhibit the attachment of osteoclasts to bone. They inhibit angiogenesis, metastasis of tumours and migration of smooth muscle cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                High affinity integrin binding peptides - can be used to attach cells to a substrate, inhibit the attachment of osteoclasts to bone, promote wound healing, inhibit angiogenesis, metastasis of tumours and migration of smooth muscle cells.
                                                                                                                                                                                                                                            High affinity; integrin binding peptide; alphas/beta1; alphav/beta5; alphav/beta3; RGD; stable configuration; wound healing; osteoclast attachemnt; bone; angiogenesis; metastasis; tumour; smooth muscle cell migration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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100.0%; Pred. No. 1.4e+06;
ive 0; Mismatches 0;
                                                                                                                                                                                                              Alpha5/betal integrin binding peptide #20.
                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers 1..5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (LJOL-) LA JOLLA CANCER RES FOUND.
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                                                                                                                AAR79093 standard; peptide; 5 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94WO-US013542
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94US-00286861
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Best Local Similarity
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                                                                                                                                                                               24-JAN-1996
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                                                                                                                                                                                                                                                                                                                                  Synthetic
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Matches
                                                                               RESULT 8
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Conservative

Local Similarity

Best Loca Matches

Query Match

cell culture body.

10-APR-1991

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To residue homocys1 is attached Acetyl and to residue Cys5 is attached NH2. The peptide is prepd. using standard methods of solid phase Synthesis and is one of 17 pref. examples of a highly generic formula. The peptide is used to inhibit fibrinogen-induced platelet aggregation and is partic. useful because it does not significantly deplete the platelet count. It has a relatively short duration of activity and is thus useful where prevention of platelet aggregation over a short period of time is desirable, e.g. in surgery of peripheral arteries and cardiovascular surgery. It is also useful in prevention of platelet thrombosis, thromboempolism and reocclusion either during and after thrombolytic therapy, or after angioplasty of coronary and other arteries and after coronary artery by-pass procedures, or to prevent myocardial confirmation. It may be combined with thrombolytic agents, e.g. plasminogen activators or streptokinase, or anticoagulants. See also AARIO413-18 and EP-410537, EP-410539, EP-410540, EP-410541, and EP-410767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New fibrinogen receptor antagonising peptide cpds. - used to inhibit blood platelet aggregation during surgery on peripheral arteries and in cardiovascular surgery.
                                                                              Fibrinogen receptor antagonist; platelet aggregation; thrombosis; myocardial infarction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic; cell migration; inhibitor; cell adhesion membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       h Similarity 100.0%; Score 35; DB 2; Length 5; Similarity 100.0%; Pred. No. 1.4e+06; 5; Conservative 0; Mismatches 0; Indels
                                               Fibrinogen receptor antagonising peptide (VI).
                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR27031 standard; peptide; 5 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 7; Page 10; 10pp; English.
                                                                                                                                                                                                              /label= homoCys
                                                                                                                                                                                                                                                                                                                                                                                                         Nutt RF, Brady SF, Veber DF,
                                                                                                                                                                                                                                                                                                             90EP-00202015.
                                                                                                                                                                                                                                                                                                                                               89US-00386534
               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                           (MERI ) MERCK & CO INC
                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1991-030928/05.
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                                                                                                                                                           Key
Disulfide-bond
Modified-site
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                                                                                                                                                                                                                                                                                                            23-JUL-1990;
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                                                                                                                                                                                                                                                                             30-JAN-1991.
                                                                                                                                                                                                                                             EP410537-A
                                                                                                                                 Synthetic
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The peptide sequence is an example of a highly generic sequence contg. the RGD motif. Compounds contg. these lipid peptides are useful as cell migration inhibitors in cell adhesion membranes or cell culture bodies. See also AAR27027-33
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                                                                                                                                                                                                                         New synthetic peptide lipid(s) and salts - useful as cell migration inhibitors, cell adhesion membranes or cell culture bodies.
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                                                                                                                                                                                                                                                                                                                                              100.0%; Score 35; DB 2; Length 5; 100.0%; Pred. No. 1.4e+06; ive 0; Mismatches 0; Indels
                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                               /note= "alkylated"
                                                                                                                                                                                                                                                     Disclosure; Page 3; 9pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "alkylated"
                                                            'note= "acylated"
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                                                                                                                                                                                 (FUJF ) FUJI PHOTO FILM CO LTD
                                                                                                                                         90JP-00333336.
                                                                                                                                                             90JP-00289494.
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                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide lipid contg.
                                                                                                                                                                                                      VPI; 1992-313679/38
                                                                                                                                                                                                                                                                                                                                                                                     1 CRGDC 5
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                                                                                                                      11-AUG-1992.
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                     Synthetic
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AAR29052
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(FUJF ) FUJI PHOTO FILM CO LTD.

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Gaps

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receptor antagonist; platelet aggregation; thrombosis; infarction.

Fibrinogen myocardial

Synthetic

Location/Qualifiers

Disulfide-bond

EP410537-A.

Fibrinogen receptor antagonising peptide (II).

(first entry)

10-APR-1991

AAR10414;

AAR10414 standard; protein; 5 AA.

RESULT 3

AAR10414 ID AA

CRGDC 5

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To residue N-MethylCysl is attached Acetyl and to residue Cys5 is attached OH. The peptide is prepd. using standard methods of solid phase synthesis and is one of 17 pref. examples of a highly generic formula. The peptide is used to inhibit fibrinogen-induced platelet aggregation and is partic. useful because it does not significantly deplete the count. It has a relatively short duration of activity and is thus useful where prevention of platelet aggregation over a short period of time is desirable, e.g. in aurgery of peripheral arteries and catdiovascular surgery. It is also useful in prevention of platelet thrombosis, thromboembolism and reocclusion either during and after thrombolytic therapy, or after angioplasty of coronary and other arteries and after coronary artery by-pass procedures, or to prevent myocardial confirmators or streptokinase, or anticoagulants. See also AARIO413-18 and activators or streptokinase, or anticoagulants. See also AARIO413-18 and EP-410537, EP-410539, EP-410540, EP-410541, and EP-410767
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New fibrinogen receptor antagonising peptide cpds. - used to inhibit blood platelet aggregation during surgery on peripheral arteries and in cardiovascular surgery.
                                  Gaps
                                                                                                                                                                                                                                                                                                                  receptor antagonist; platelet aggregation; thrombosis;
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   Length 5;
100.0%; Score 35; DB 2; Length 5; larity 100.0%; Pred. No. 1.4e+06; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                 Fibrinogen receptor antagonising peptide (III).
                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= N-MethylCys
                                                                                                                                                                                 AAR10415 standard; protein; 5 AA
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                                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                Fibrinogen receptor ar
myocardial infarction.
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 Query Match
Best Local Similarity
Matches 5; Conserv
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Modified-site
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                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
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To residue Cys5 is attached OH. The peptide is prepd. using standard methods of solid phase synthesis and is one of 17 pref. examples of a highly generic formula. The peptide is used to inhibit fibrinogen-induced platelet aggregation and is partic. useful because it does not significantly deplete the platelet count. It has a relatively short duration of activity and is thus useful where prevention of platelet aggregation over a short period of time is desirable, e.g. in surgery of peripheral arteries and cardiovascular surgery. It is also useful in prevention of platelet thrombosis, thromboembolism and reocclusion either during and after thrombolytic therapy, or after angioplasty of coronary and other arteries and after connary attery by-pass procedures, or to prevent myocardial infarction. It may be combined with thrombolytic agents, e.g. plaaminogen activators or streptokinase, or anticoagulants.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                agents, e.g. plasminogen activators or streptokinase, or anticoagulants. See also AAR10413-18 and EP-410537, EP-410539, EP-410540, EP-410541, and EP-410767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                New fibrinogen receptor antagonising peptide cpds. - used to inhibit blood platelet aggregation during surgery on peripheral arteries and in cardiovascular surgery.
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100.0%; Pred. No. 1.4e+06;
ive 0; Mismatches 0;
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100.0%; Score 35; DB 2; Length 5; 100.0%; Pred. No. 1.4e+06; ative 0; Mismatches 0; Indels

5; Conservative

Query Match Best Local Similarity Matches 5; Conserv

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September 22, 2004, 07:48:21; Search time 121 Seconds (without alignments) 11.676 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                  1586107 segs, 282547505 residues
                                                               OM protein - protein search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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1: geneseqp1980s:*

2: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2003s:*

6: geneseqp2003as:*

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8: geneseqp2003as:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	1	Aarll587 Fibrinoge	Aar10415 Fibrinoge					Aar69325 Gp IIb/II	Aar79093 Alpha5/be	Aaw03492 Alpha(5)-	Aaw48499 Integrin	Aaw64952 Targettin	Aaw50594 GPIID/III				Aay95465 GPIID/III		Abu59650 Finbronec	Aay16025 Snake ven					SVat	00
SUMMARIES		AAKIIS8/	AAR10415	AAR10414	AAR10418	AAR27031	AAR29052	AAR69325	AAR79093	AAW03492	AAW48499	AAW64952	AAW50594	AAY21570	ADE25491	AAY54976	AAY95465	AAE17982	ABU59650	AAY16025	AA022876	AAB97087	ABP54052	ABG70730	AAU79139	AAG78428
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                        STRAIN=Gunn;
MEDLINE=91282758; PubMed=1840486;
Sato H., Anno S., Kashiwamata S., Koiwai O.;
Genetic defect of bilirubin UDP-glucuronosyltransferase in the hyperbilirubinemic Gunn rat.";
Blochem Biophys. Res. Commun. 177:1161-1164 (1991).
EMBL; S38656; AAB19259.1;
GQ; GQ:0016740; F:transferase activity; IEA.
                              008433;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Bilirubin UDP-glucuronosyltransferase (Fragment).
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Similarity 0.0%; I
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"ILME: a waterborne pheromonal peptide released by the eggs of Sepia
                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Mollusca, Cephalopoda, Coleoidea, Neocoleoidea,
Decapodiformes, Sepioidea, Sepiidae, Sepia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zatylny C., Marvin L., Gagnon J., Henry J.;

"Fertilization in Sepia officinalis: the first mollusk sperm-
attracting peptide.";

Biochem. Biophys. Res. Commun. 296:1186-1193 (2002).

-!- SUBCELLUIAR LOCATION: BEREETED.

-!- TISSUE SPECIFICITY: FOLLICLE, FULLY GROWN OOCYTE AND EGG(EC2).

-!- MASS SPECIFICITY: WW=505.4; METHOD=MALDI.

GO; GO:0005186; F:pheromone activity; IEA.
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                                                                                                                                                                                                    14.3%; Score 5; DB 13; Length 5; 100.0%; Pred. No. 1e+06; ative 0; Mismatches 0; Indels
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Pred. No. 1e+06;
1; Mismatches 0; Indela
                                                                                                                                             GO; GO:0007218; P:neuropeptide signaling pathway; TAS Neuropeptide; Amidation.

AMIDATION.
                                                                                                                                                                                                                                                                                                                                                       01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                     5 5 AMIDATION.
5 AA; 645 MW; 69D4073767400000 CRC64;
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                                                                                                                                                                                                                                                                                                                                    4 AA.
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Sepia officinalis (Common cuttlefish).
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0.0%; I
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Best Local Similarity 100...
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                                SEQUENCE, AND SYNTHESIS
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PubMed=12207899;
       NCBI_TaxID=9031;
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P83568;
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Score 2; DB 11; Length 4; Pred. No. 1e+06; 1; Mismatches 0; Indels

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                                                                                                                                         Hordeum vulgare (Barley).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae;
Triticeae; Hordeum.
NCBI_TaxID=4513;
                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDINGE-1831055;
MEDINTRE-91229704; PubMed-1831055;
MACOLINE-91229704; PubMed-1831055;
"Control of transient expression of chimaeric genes by gibberellic acid and abscisic acid in protoplasts prepared from mature bareley
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Pred. No. 1e+06;
1; Mismatches 0; Indels
                                                             Last sequence update)
Last annotation update)
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BMBL; X54643; CAA38455.1; -.

NON TER

SEQUENCE 5 AA; 600 MW; 61E3344DD6F00000 CRC64;
5 AA.
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                                            Created)
PRT;
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Similarity 0.0%; 1
0; Conservative 1
                                        01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-MAR-2003 (TrEMBLrel. 23, Alpha amylase (Fragment).
PRELIMINARY;
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P83568 sepia offic
Q08433 rattus sp.
Q99007 hordeum vul
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P83073 bacillus ce
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14.213 Million cell updates/sec
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                                                             September 22, 2004, 07:02:58 ; Search time 111 Seconds
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    GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 1008
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                                         - protein search, using sw model
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P83073
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P83568
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Q99007
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Gapop 10.0 , Gapext 0.5
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Database :

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P89308 PRELIMINARY; PRT; 5 AA.
P89308 D1-JUN-2002 (TTEMBLERE1. 21, Last sequence update)
01-JUN-2002 (TTEMBLERE1. 21, Last sequence update)
01-JUN-2003 (TTEMBLERE1. 24, Last annotation update)
01-JUN-2003 (TTEMBLERE1. 21, Last sequence)
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                                                                                                                                      Eukaryota, Metazoa, Mollusca, Cephalopoda, Coleoidea, Neocoleoidea, Decapodiformes, Sepioidea, Sepiidae, Sepia. NCBI_TaxID=6610,
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1; Conservative 0; Mismatches 0; Indels
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P83072-2001 (TrEMBLrel. 18, Created)
01-0CT-2001 (TrEMBLrel. 18, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
88 kDa protein (Fragment).
Bacillus cereus.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI _TAXID=1396;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Neuropegride GWa.
Sepia officinalis (Common cuttlefish).
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2 AA; 261 MW; 737810000000000 CRC64;
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17.1%; Score 6; DB 5; L
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 1; Conservative 0; Mismatches 0
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STRAIN-NCIMB 11796;
Browne N., Dowds B.C.A.;
Submitted (JUL-2001) to Swiss-Prot.
                                                                                                                                                                                                                                                                                                                      TISSUE=Optic lobe;
PubMed=9437704;
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P83308
LD P8333
DT 01-J
DT 01-J
DE FMRF
OS GA11
OC EUKA
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RESULT 1

P83570

Result Š.

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Pelodryadinae, Litoria.
            NCBI_TaxID=104895;
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RE32_LITRU
ID RE32_LITRU
AC P82073;
                                                                                                                                                                                                                            Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Skin secretion;
MEDLINE-87057369; PubMed=3782138;
Lazarovici P., Primor N., Loew L.M.;
"Purification and pore-forming activity of two hydrophobic polypeptides from the secretion of the Red sea moses sole (Pardachirus
                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J. Biol. Chem. 261:16704-16713(1986).
-!- FUNCTION: Exhibits unusual shark repellent and surfactant
properties. Forms voltage-dependent, ion-permeable channels
in membranes. At high concentration causes cell membrane lysis.
                                                                                                                                                                                                                                                                                                       28-FEB-2003 (Rel. 41, Last annotation update)
Bardaxin II (PKII) (Fragment).
Pardachirus marmoratus (Red sea moses sole).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Taleostei; Buteleostei; Neoteleosteis
Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
Soleoidei; Soleidae; Pardachirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Litoria rubella (Desert tree frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Neobatrachia, Hyloidea, Hylidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SUBUNIT: Monomer. In aqueous solution exists as a tetramer.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the pardaxin family.
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                                                                                                                                                     0; Indels
                                                                                                                               DB 1; Length 5;
                                           Interpro; IPR005814; Aminotrans 3.
PROSITE; PS00600; AA TRANSPER CLASS 3; PARTIAL.
Biotin biosynthesis; Transferase; Aminotransferase;
                                                                                                     SEQUENCE 5 AA; 582 MW; 6AAAB1B1A6F00000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 AA; 614 MW; 7769C9C9C8100000 CRC64;
                                                                                                                            Score 6; DB 1; Ler
Pred. No. 1.4e+05;
                                                                                                                                                                                                                                                                              30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                   17.1%; Scor.
100.0%; Pred. No. ...
0; Mismatches
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28-FEB-2003 (Rel. 41, Last sequence update)
20-CCT-2003 (Rel. 42, Last annotation update)
Rubellidin 1.1.
                                                                                                                                                                                                                                                             5 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 AA
send an email to license@isb-sib.ch).
                       EMBL; M21922; -; NOT ANNOTATED_CDS.
PIR; 140697; 140697.
                                                                                                                                                                                                                                                             PRT;
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                                                                                                                 Query Match
Best Local Similarity 100.00
best Local 1, Conservative
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Best Local Similarity 100.
Matches 1, Conservative
                                                                                                                                                                                                                                                             STANDARD;
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                                                                             Pyridoxal phosphate.
NON_TER 5
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P82070;
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SEQUENCE
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PAP2 PARMA
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                      TISSUE-Skin secretion, Steinborner S.T., Waugh R.J., Bowie J.H., Gao C., Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C., Tyler M.J., Wallace J.C., Tyler M.J., Wallace J.C., "The structure of new peptides from the Australin red tree frog 'Litoria rubella'. The skin peptide profile as a probe for the study of evolutionary trends of amphibians."; Aust. J. Chem. 49:955-961(1996).
-I- FUNCTION: Shows neither neuropeptide activity nor antibiotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
Pelodryadinae; Litoria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rubella.";
Aust. J. Chem. 52:639-645(1999).
-!- FUNCTION: Shows neither neuropeptide activity nor antibiotic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                      -i- TISSUE SPECIFICITY: Expressed by the skin dorsal glands
-i- MASS SPECIROMETRY: WW=598; METHOD=FAB.
Amphibian defense peptide.
SEQUENCE 5 AA; 598 MW; 6DD9C9CAB2A00000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SUBCELLÚLAR LOCATION: Secreted.
1- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
Amphibian defense peptide.
SEQUENCE 5 AA, 570 MW; 71A9C9C862A00000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
"Peptides from the skin glands of the Australian buzzing
Litori electrica. Comparison with the skin peptides from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17.1%; Score 6; DB 1; Length 5; 100.0%; Pred. No. 1.46+05; trive 0; Mismatches 0; Indel:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17.1%; Score 6; DB 1; Length 5; 100.0%; Pred. No. 1.4e+05; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-FBB-2003 (Rel. 41, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Rubellidin 3 2.
Ritoria rubella (Desert tree frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 AA.
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Job time : 23 secs
                                                                                                                                                                                                                                                                               activity.
SEQUENCE, AND MASS SPECTROMETRY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-FEB-2003 (Rel. 41, Created)
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1; Conservative
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- COFACTOR: Pyridoxal phosphate.
-!- PATHWAXT: Biotin biosynthesis.
-!- SUBUNIT: Homodimer.
-!- SIMILARITY: Belongs to class-III of pyridoxal-phosphate-dependent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Adenosylmethionine-8-amino-7-oxononanoate aminotransferase
(RC 2.6.1.62) (7,8-diamino-pelargonic acid aminotransferase) (DAPA aminotransferase) (PAPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Citrobacter,
                                                                                                                                                                                                                                                                                                                                                                                                        Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
                                                                                                                                                    Carcinus maenas (Common shore crab) (Green crab).
Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
Bumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
Eubrachyura; Portunoidea; Portunidae; Carcinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 5;
                                                                                                                                                                                                                                                                                                                  TISSUB-Cerebral ganglion, and Thoracic ganglion, MEDLINE=98121193; Pubmed=9461295;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.4e+05;
                                                                                          30-MAY-2000 (Rel. 39, Last sequence update) 30-MAY-2000 (Rel. 39, Last annotation update)
                       5 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17.1%; Score 6; DB 1
100.0%; Pred. No. 1.4
tive 0; Mismatches
                                                                  (Rel. 39, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 100.
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                       STANDARD;
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                                                                                                                                          Carcinustatin 14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=546;
                                                                  30-MAY-2000
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                                                                                                                                                                                                                                                                                                   SEQUENCE
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P13071;
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MEDLINE=7678412; PubWed=1060093;

Goetzl E.U., Austen K.F.;

"Purification and synthesis of eosinophilotactic tetrapeptides of numan lung tissue: identification as eosinophil chemotactic factor of anaphylaxis.";

"Proc. Natl. Acad. Sci. U.S.A. 72:4123-4127(1975).

"In Proc. Natl. Acad. Sci. U.S.A. 72:4123-4127(1975).

"In MSCELLANEOUS: These peptides are released from mast cells in lung during buring hyptacensity reactions (anaphylaxis). Their activities, preferentially affecting eosinophils, include chemotaxis, chemotactic deactivation, release of enzymes, and stimulation of the hexose monophosphate shunt.

GO; GO:0006935; P:chemotaxis; IDA.

GO; GO:0006955; P:immune response; IDA.

YORANT IN VARIANT IN VARIANT | V-SA (IN OTHER PEPTIDE).
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Octopodiformes, Octopoda, Incirrata, Octopodidae, Octopus
                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17.1%; Score 6; DB 1; Length 4; 100.0%; Pred. No. 1.46+05; ative 0; Mismatches 0; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 2 D-SERINE (IN OCP-4).
4 AA; 463 MW; 6AB365B810000000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.4e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        active than Ocp-3.
-!- SUBCELLULAR LOCATION: Secreted.
-!- PTM: Ocp-4 has D-Ser instead of L-Ser.
-!- MASS SPECTROMETRY: MW=395.2; METHOD=MALDI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17.1%; Score 6; DB 1
100.0%; Pred. No. 1.4
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Brain;
MEDLINE=20336815; PubMed=10876044;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cardioactive peptides Ocp-3/Ocp-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-FEB-2003 (Rel. 41, Created)
Eosinophilotactic peptides.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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                                                                                             NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                      site for the lux operon.";
J. Bacteriol. 172:6797-6802(1990).
-!- FUNCTION: ACYL-PROTEIN SYNTHETASE ACTIVATES TETRADECANOIC ACID.
IT IS A COMPONENT OF THE FATTY ACID REDUCTASE COMPLEX RESPONSIBLE FOR CONVERTING TETRADECANOIC ACID TO THE ALDEHYDE WHICH SERVES AS SUBSTRATE IN THE LUCIFERASE-CATALYZED REACTION.
-!- CATALYTIC ACTIVITY: ATP + an acid + protein = AMP + diphosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Achatina fulica (Giant African snail).
Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
Sigmurethra; Achatinoidea; Achatinidae; Achatina.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                an acyl-protein thiolester.
-!- PATHWAY: Bioluminescent fatty acid reduction system; second step.
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                                                                                                                                                                         Swartzman E., Kapoor S., Graham A.F., Meighen E.A.;
"A new Vibrio fischeri lux gene precedes a bidirectional termination
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MEDLINE=82273551; PubMed=2597281;
Kamatani Y., Minakata H., Kenny P.T.M., Iwashita T., Watanabe K.,
Funase K., Sun X.P., Yongairi A., Kim K.H., Novales-Li P.,
Novales E.T., Kanapi C.G., Takeuchi H., Nomoto K.;
"Acharin-I, an endogenous neuroexcitatory tetrapeptide from Achatina fulica Ferussac containing a D-amino acid residue.";
Biochem. Biophys. Res. Commun. 160:1015-1020(1989).
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01-JUN-1994 (Rel. 29, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
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Luminescence; Ligase.
                                                                                                                                     MEDLINE=91072226; PubMed=2254256;
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   Vibrionaceae, Vibrio
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                                    NCBI_TaxID=668;
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P35904;
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                                                                          D-amino acid residue.";
Int. J. Pept. Protein Res. 39:258-264(1992).
-I- FUNCTION: Neuroexcitatory peptide, increases the impulse frequency and produces a spike broadening of the identified heart excitatory neuron (PON); also enhances the amplitude and frequency of the heart beat. Has also an effect on several other muscles.

PIR: A32480; A32480.
Hormone; D-amino acid.
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-!- SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND
                                                                                                                                                                                                                                                                                                                                                                                                                      Gарв
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Iwashita T., Nomoto K.;
"Crystal structure and molecular conformation of achatin-I
(H-Gly-D-Phe-Ala-Asp-OH), an endogenous neuropeptide containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kraut M., Hugendieck I., Herwig S., Meyer O.;
"Homology and distribution of CO dehydrogenase structural genes
carboxydotrophic bacteria.";
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Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae.
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5. 1.4e+05;
cches 0; Indels
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01-FEB-1991 (Rel. 17, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Carbon monoxide dehydrogenase large chain (EC 1.2.99.2)
dehydrogenase subunit L) (CO-DH L) (Fragment)
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tive 0; Mismatches
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MEDLINE=98163340; PubMed=9504812;
Dunn M.J., Corbett J.M., Wheeler C.H.;
"HSC-2DPAGE and the two-dimensional gel electrophoresis database of dog heart proteins.";
Electrophoresis 18:2795-2802(1997).
-1- CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate = glycerone
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Best Local Similarity
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P24272;
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GRWM_HUMAN
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J. Bacteriol. 170:2749-2757(1988).
-!- FUNCTION: TRANSER GENE PROTEIN. IS INVOLVED IN THE CONJUGATION
PROCESS OF BACTERIAL CELLS FOR THE EXCHANGE OF PLASMID DNA.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-88227859; PubMed-2836369;
Inamoto S., Yoshioka Y., Ohtsubo E.;
"Identification and characterization of the products from the traJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Canis familiaris (Dog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Carnivora, Fissipedia, Canidae, Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria, Proteobacteria, Gammaproteobacteria; Enterobacteriales,
Enterobacteriaceae; Escherichia.
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0
                Score 12; DB 1; Length 5;
Pred. No. 1.4e+05;
                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Triosephosphate isomerase (EC 5.3.1.1) (TIM) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22.9%; Score 8; DB 1; Length 5; 33.3%; Pred. No. 1.4e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 AA; 634 MW; 6B1B1AA443500000 CRC64;
                                                                                                                                                                                                                                                                       01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
34.3%; Scor.
100.0%; Pred. No. ...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 AA.
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PIR, A32014; A32014.
Conjugation; Plasmid, DNA-binding.
NON_TER
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                                                        Conservative
                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                      TraM protein (Fragment)
                                                                                                                                                                                                                                                                                                                                                                            Escherichia coli.
Plasmid IncFII R100.
                             Best Local Similarity
Matches 2, Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=562;
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P54714;
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SEQUENCE.
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Matches
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01-MAR-1992 (Rel. 21, Last sequence update)
01-OT-1996 (Rel. 34, Last annotation update)
Long-chain-fatty-acid-lucide-in-component ligase (EC 6.2.1.19) (Acyl-protein synthetase) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-77162369; PubMed-858356; Schlesinger D.H., Pickart L., Thaler M.M.; Schlesinger D.H., Pickart L., Thaler M.M.; Growth-modulating serum tripeptide is glycyl-histidyl-lysine."; Growth-modulating aserum tripeptide is glycyl-histidyl-lysine."; -!- MISCELLANEOUS: This serum tripeptide has been found to stimulate growth of some cell types and to inhibit other types in vitro. GO; GO:001558; P:regulation of cell growth; NAS. SEQUENCE 3 AA; 340 MM; 6331E81000000000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                  Length 5;
                                                                                                                                                                                                                                                                             5 AA; 550 MW; 64444862C9A00000 CRC64;
                                                                                                                                                                                                                                                                                                                               20.0%; Score 7; DB 1; L 50.0%; Pred. No. 1.4e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-1986 (Rel. 01, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 AA.
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P58648 octopus min
P38005 chlamydia t
P13973 escherichia
P54714 canis famil
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hirudo medi
hirudo medi
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                                                       September 22, 2004, 07:02:23; Search time 22 Seconds (without alignments) 11.834 Million cell updates/sec
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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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OCP3_OCTMI
ALIJ_CARMA
BIOA_CITFR
REII_LITRU
RE32_LITRU
UF01_MOUSE
FAR3_HIRME
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Maximum Match 100%
Listing first 45 summaries
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ACH1 ACHFU
DCML PSECH
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PSK DAUCA
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Gapop 10.0 , Gapext 0.5
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35
1 CRGDC 5
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Match Length
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P36515 saccharomyc
P12997 citrobacter
P82099 litoria rub
P82100 litoria rub
P19991 acheta dome
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                                                                                                                                            28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2004 (Rel. 41, Last annotation update)
Cardioactive peptides Ocp-1/Ocp-2.
Octopus minor (Octopus).
Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neccoleoidea; Octopodiformes; Octopoda; Incirrata; Octopodidae; Octopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pallini V.;
Submitted (SEP-1994) to Swiss-Prot.
-- MISCELLANBOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
PROTEIN IS: 4.5, ITS MW IS: 28 kDa.
Siena-2DPAGE; P38005; --
NOW TER
S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE.
STRAIN=L2/434/Bu;
STRAIN=L2/434/Bu;
Bini L., Santucci A., Magi B., Marzocchi B., Sanchez-Campillo M.,
Comanducci M., Christianen G., Birkelund S., Vtretou E., Ratti G.
                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                           SEQUENCE, SYNTHESIS, MASS SPECTROMETRY, AND CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-0CT-1994 (Rel. 30, Created)
01-0CT-1994 (Rel. 30, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Unknown protein from 2D-page from elementary body (Fragment)
Chlamydia trachomatis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
NCBI_TaxID=813;
                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 34.3%; Score 12; DB 1; Length 4; Best Local Similarity 100.0%; Pred. No. 1.4e+05; Matches 2; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                           2 2 D-PHENYLALANINE (IN OCP-1)
4 AA; 394 MW; 6AA879C810000000 CRC64;
                                                                                                                            4 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 AA.
                                                                        ALIGNMENTS
RM01_YEAST
BIOB_CITFR
EI03_LITRU
EI04_LITRU
SUGA_ACHDO
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ID UXA4_CHLTR
AC P38005;
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OM protein - protein search, using sw model

Run on:

September 22, 2004, 07:04:09; Search time 38 Seconds (without alignments) 12.657 Million cell updates/sec

US-09-912-609-9 35 1 CRGDC 5

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 segs, 96191526 residues Searched:

206 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 5

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 78:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES Rea

		æ			SOUTHERIES	
sault No.	Score	ta	Length		۵	scription
-	17	48.6		2	B45525	actin I - malaria
7	14	40.0	4	7	95	Ig mu chain V regi
Э	14	40.0	ιO	7	F22565	R-phycoerythrin ga
4	12	34.3	4	7	PT0711	tor
Ŋ	12	34.3	S	~	PQ0689	photosystem I 10.4
9	12	34.3	S	0	PT0513	T-cell receptor be
7	12	34.3	S	~	PT0538	T-cell receptor be
œ	12	34.3	ιΩ	~	PT0703	-cell receptor
0	12	34.3	ß	N	PT0690	_
10	12	34.3	ß	~	PT0573	_
11	12	34.3	S	7	PT0679	T-cell receptor be
12	11	31.4	4	7	S47552	ubiquitin - rat
13	11	31.4	4	7	S55238	pallidipin - assas
14	11	31.4	S	7	A33882	cadmium-binding pe
15	11	31.4	ហ	~	PT0525	T-cell receptor be
16	11	31.4	S	~	PT0608	-cell
17	11	31.4	ß	~	PT0695	T-cell receptor be
18	11	31.4	S	~	PT0700	T-cell receptor be
19	6	25.7	m	m	A22565	R-phycoerythrin al
20	O	25.7	4	~	IS1049	metallothionein-A
21	σ	25.7	S	N	B22565	R-phycoerythrin al
22	σ	25.7	2	7	865726	hemoglobin, extrac
23	80	22.9	4	~	D41654	hypothetical prote
24	80	ö	4	7	PT0677	ll recept
25	ω	ď	2	0	A32014	10
56	œ	22.9	D.	~	PT0540	T-cell receptor be
27	7	ö	m	m	A23751	spinal cord peptid
28	7	ö	4	-	ECXAA	RFami
29	7	20.0	4	7	A25844	autho-RF amide neu

globulin IV alpha growth-modulating bursin - chicken spinal cord peptid T-cell receptor be tyrosine-melanocyt carbon-monoxide de biotin A - Citroba protein D - Escher hypothetical prote COI intron 16 prot RPCH-related neuro achatin I - giant myosin-light-chain	Ig heavy chain CRD
S09478 GKHU A60898 B23751 PT0636 PT0571 A32039 PL0140 I40697 A41890 T30569 I38888 A34626 A34626	PT0240
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0 1 1 2 1 2 1 2 1 2 1 2 1 2 1 2 1 2 1 2	45

## ALIGNMENTS

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C;Species: Plasmodium falciparum
C;Date: 03-Jun-1903 #sequence_revision 28-Oct-1994 #text_change 09-Jun-2000
C;Accessino: B4525 #sequence_revision 28-Oct-1994 #text_change 09-Jun-2000
C;Accessino: B4525 #sequence_revision 28-Oct-1994 #text_change 09-Jun-2000
C;Accessino: B4525 #sequence_revision and genomic organization of the actin genes of the mal A;Reference number: A4525; MUID:89364996; PMID:2671721
A;Accession: B4525
A;Gatus: Preliminary
A;Molecule type: DNA
A;Residues: 1-5 <WES>
A;Cross-references GB:J03988
A;Note: the authors translated the codon GAA for residue 3 as Gly
C;Comment: The actin I gene contains no introns.
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Crispecies: All sapiens (man)
Crispecies: All sapiens (man)
Crispecies: S.D.; Williams, G.T.; Larson, T.; Neuberger, M.S.; Kitamura, D.; Rajewsky, K.; Nucleic Acids Res. 22, 1389-1393, 1994
All sapiens (man)
Crispecies: Likely (Man)
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actin I - malaria parasite (Plasmodium falciparum) (fragments)
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Best Local Similarity 66.7
Matches 2; Conservative
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Matches 2; Conserv
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RESULT 3

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Gaps

1; Indels

Score 14; DB 2; Length 5; Pred. No. 2.8e+05; 0; Mismatches 1; Indels

40.0%;

Best Local Similarity 66.7 Matches 2; Conservative

Query Match

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C;Accession: PQ0689
R;Obokata, J.; Mikami, K.; Hayashida, N.; Nakamura, M.; Sugiura, M.
P;Obokata, J.; Mikami, K.; Hayashida, N.; Nakamura, M.; Sugiura, M.
Plant Physiol. 1829-1259-1267, 1959
A;Title: Molecular heterogeneity of photosystem I. psaD, psaE, psaF, psaH and psaL are al. A;Reference number: PQ0667; MUID:94105345; PMID:8278548
A;Accession: PQ0689
A;Aolecule type: protein
A;Residues: 1-5 <OBO>
C;Keywords: chloroplast; photosynthesis; photosystem I; thylakoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Accession: PT0513; PT0606
R; Peeney, A.J.
J; Exportional sequence_revision 17-Jul-1992 #text_change 30-May-1997
C; Pacession: PT0513; PT0606
R; Peeney, A.J.
J; Exportional sequence of fetal T cell receptor beta chains have few N regions. A; Reference number: PT0509; MUD:91277601; PMID:1711558
A; Retens: pT0513
A; Retens: pT05
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A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
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C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0538; PT0539; PT0603
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A;Residues: 1-5 <FEE>
A;Experimental source: day 18 fetal thymus, strain BALB/c, clone 126-1F
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A;Experimental source: newborn thymus, strain BALB/c, clone 120-1S
C;Keywords: T-cell receptor
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A;Status: translation not shown
A;Molecule type: mRNA
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2; Conservative
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A; Residues: 1-5 < FE3>
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Best Local S:
Matches 2,
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PT0711

C. Feel receptor beta chain V-D-J region (120-2J) - mouse (fragment)

C. Species: Mus musculus (house mouse)
C. Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C. Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A. Feeney, A.J.
A.
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A/Status: translation not shown
A/Status: translation not shown
A/Molecule type: DNA
A/Residues: 1-4 <FES>
A/Experimental source: newborn thymus, strain BALB/c (clones 161-2AE and 161-2AF)
C/Keywords: T-cell receptor
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                 F-phycoerythrin gamma-A chain - red alga (Gastroclonium coulteri) (fragment) C.Species: Gastroclonium coulteri C.Species: Gastroclonium coulteri C.Species: 07-Mar-1988 #sequence_revision 07-Mar-1988 #text_change 23-Mar-1993 C.Accesion: F22565
R.Klotz, A.V.; Glazer, A.N.
J. Biol. Chem. 260, 4856-4863, 1985
A.Fitle: Characterization of the bilin attachment sites in R-phycoerythrin. A.Reference number: A22565; MUID:85182601; PMID:3866644
A.Accession: F22565
A.Molecule type: protein
A.Residues: 1-5 <KLO>
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photosystem I 10.4K H1 chain - common tobacco (fragment)
C;Species: Nicotiana tabacum (common tobacco)
C;Dete: 19-May-1994 #sequence_revision 19-May-1994 #text_change 17-Mar-1999
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A,Residues: 1-4 <FE2>
A,Experimental source: day 18 fetal thymus, strain BALB/c, 140-1G
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A;Experimental source: day 19 fetal thymus, strain BALB/c, 141-11
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A, Experimental source: newborn thymus, strain BALB/c, 120-2J

A; Accession: PT0674
A; Status: translation not shown

A;Status: translation not shown A;Molecule type: mRNA A;Residues: 1-4 <FE1>

strain BALB/c,

A;Status: translation not shown A;Molecule type: DNA A;Residues: 1-4 <FE3> A;Experimental source: day 18 fetal thymus,

A; Accession: PT0678

A; Accession: PT0570
A; Status: translation not shown A; Molecule type: mRNA

34.3%; Score 12; DB 2; Length 4; 100.0%; Pred. No. 2.8e+05; tive 0; Mismatches 0; Indels

Query Match
Best Local Similarity 100.
Matches 2; Conservative

RESULT 5

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Cispecies: Rattus norvegicus (Norway rat)
Cispecies: Rattus norvegicus (Norway rat)
Cispecies: Rattus possible sequence_revision 21-Jul-1995 #text_change 17-Mar-1999
Cispecession: 847552
Cispecession: 847552
Biochim. Biophys. Acta 1200, 191-196, 1994
Airlie: Differential feeding-related regulation of ubiquitin and calbindin(9kDa) in rat
Airle: Differential feeding-related regulation of abiquitin and calbindin(9kDa) in rat
Airle: Differential feeding-related regulation
Airle: Differential feeding-related regulation of abiquitin and calbindin(9kDa) in rat
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Airle: Differential feeding-related regulation of abiquitin and calbindin(9kDa) in rat
Airle: Differential feeding-related regulation of abiquitin and calbindin(9kDa) in rat
A,Title: Junctional sequences of fetal T cell receptor beta chains have few N regions. A,Reference number: PT0509; MUD:91277601; PMID:1711558
A,Accession: PT0573
A,Accession: PT0573
A,Status: translation not shown
A,Molecule type: mRNA
A,Residues: 1-5 eFEE>
A,Experimental source: day 19 fetal thymus, strain BALB/c
C,Keywords: T-cell receptor
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A.Fitle: Junctional-sequences of fetal T cell receptor beta chains have few N regions.
A.Referenmeer number: PT0509; MUID:91277601; PMID:1711558
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C;Speciés: Mus musculus (house mouse)
C;Date: 117-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0679; PT0708
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A)Accession: PT0708
A)Astaus: translation not shown
A)Molecule type: DNA
A)Kesidues: 1-5 <FE2>
A)Experimental source: newborn thymus, strain BALB/c, 161-2B
C)Keywords: T-cell receptor
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34.3%; Score 12; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches ——27——Conservative——0; Mismatches 0; Indels
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A;Molecule_type: DNA
A;Residues: 1-5 <FEE>
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Matches 2; Conserva
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J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
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A,Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A,Reference number: PT0509; MUID:91277601; PMID:1711558
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C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accesion: PTG573
S;Feensy, A.J.
J. Exp. Med. 174, 115-124, 1991
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C;bpecies: Nus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0703
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C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0690
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                A;Residues: 1-5 <FE2>
A;Experimental source: newborn thymus, strain BALB/c, clone 100-2AC
C;Keywords: T-cell receptor
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A;Experimental source: day 18 fetal thymus, strain BALB/c
C;Keywords: T-cell receptor
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34.3%; Score 12; DB 2; Le
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0;
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A;Residues: 1-5 cFEB.
A;Experimental source: newborn thymus, strain BALB/c
C;Keywords: T-cell receptor
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Best Local Similarity 100.(
Matches 2; Conservative
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RESULT 9

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RESULT 10

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Job time : 39 secs
                                       pallidipin - assassin bug (fragment)

CiSpecies: Triatcoma pallidipennis (assassin bug)

CiSpecies: Triatcoma pallidipennis (assassin bug)

CiDate: 19-Mar-1997 #sequence_revision 18-Jul-1997 #text_change 19-May-2000

CiAccession: S55238

RiHaendler, B.; Becker, A.; Noeske-Jungblut, C.; Kraetzschmar, J.; Donner, P.; Schleunin Bicchem. J. 307, 465-407, 1995

A; Hitle: Expression of active recombinant pallidipin, a novel platelet aggregation inhib A; Reference number: S55238

A; Accession: S55238

A; Accession: S55238

A; Residues: 1-4 <HAE>
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Proc. Natl. Acad. Sci. U.S.A. 84, 6619-6623, 1987
A;Titlel: Poly(gamma-glutamylcysteinyl)glycine: its role in cadmium resistance in plant A;Reference number: A94182; MUID:88016144; PMID:3477793
A;Accession: A33882
A;Molecule type: protein
A;Residues: 1-5 < JAC>
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C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0525
R;Feeney, A.J.
J; Exp. Med. 1174, 115-124, 1991
A;Ritle: Junctional sequences of fetal T cell receptor beta chains have few N regions. A;Reference number: PT0509; MUID:91277601; PMID:1711558
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C;Species: Datura innoxia (downy thornapple)
C;Date: 21-May-1990 #sequence_revision 21-May-1990 #text_change 18-Jun-1993
C;Accession: A33882
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Pred. No. 2.8e+05;
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31.4%; Score 11; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels
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A;Molecule type: mRNA A;Residues: 1-5 <FEE>
A;Residues: 1-5 <FEE>
A;Experimental source: adult thymus, strain BALB/C
C;Keywords: T-cell receptor
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Best Local Similarity 50.0
Matches 1; Conservative
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